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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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REFERENCE AUTHORS TITLE JOURNAL

AX137747 Sequence
AX137751 Sequence
V01115 Minute viru
U03255 Minute viru
U034253 Mouse parvo
U13469 Mouse parvo
U13469 Mouse parvo
U13454 Mouse parvo
U13454 Mouse parvo
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U13455 Hamster par
M81888 Parvovirus
AF317513 Arvovirus
AF317513 Arvovirus AF33284 Rat minut X01457 Parvovirus AL60f756 Mouse DNA AL600049 Feline pa AB000049 Feline pa AB000051 Feline pa AB000055 Feline pa AB000055 Feline pa AB000056 Feline pa AB000065 Feline pa AB000069 Feline pan 1 Nucesch,J. and Rommelaere,J. Parvovirus ns1 variants Patent: EP 1077260-A 3 21-FEB-2001; Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts PAT 30-MAY-2001 AX137738 Sequence AX137739 Sequence AX137736 Sequence AX137743 Sequence AX137751 Sequence Mice minute virus Mice minute virus Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus. score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. linear DNA ALIGNMENTS AX137738 60 bp Sequence 3 from Patent EP1077260. AX137738 GI:14273911 SUMMARIES AX137743 AX137747 AX137747 AX137747 AX137747 AX137747 AX137747 AX137747 AX137747 AX137751 AX137751 AX137751 AX13751 PAFPVNS1 AR043629 AR043630 AX137739 AX137736 **PVCY1A** ū В 90.3 90.3 90.3 90.3 87.7 887.7 885.0 87.7 90.3 90.3 90.3 90.3 90.3 90.3 90.3 90.3 90.3 90.4 90.7 2019 2019 2019 2019 2019 2019 5149 4764 4761 4761 4761 4761 4761 5135 Length % Query Match 1 RESULT 1
AX137738
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PAT 30-MAY-2001

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Parvovirus ns1 variants
Batent: EP 1077260-A 8 21-PEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts (DE)
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Patent: EP 1077260-A 1 21-FEB-2001;
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Sequence 8 from Patent BP1077260.
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Sequence 1 from Patent EP1077260.
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Matches 59; Conservative
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Parvovirus nsl variants
Patent: EP 1077260-A 4 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts (DE)
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ilarity 100.0%; Pred. No. 7.8e-10;
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Patent: EP 1077260-A 12 21-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT S
AX137747
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                        CDS
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ORIGIN

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/ DECOLETI 164=CAC39997.1"

/ DECOLETI 164=CAC39997.1"

/ Ab xref="G1:14273926"

/ Ab xref="G1:14273926"

/ Ab xref="G1:14073926"

/ Ab xref="G1:14073926"

/ Aranal at ion="MAGNAYSDEDMEWETTVDEWTKRQVFIFDSLVKKCLFEVL
NTKNIFPGDELKSLQRGAETTWDQSEDMEWETTVDEWTKRQVFIFDSLVKKCLFEVL
NTKNIFPGDTWMFVQHEWGKDGWHCHVLLTYKHKQTKKDYFKCVLFGWILAYYWSFWLVTA
CNVQLTPAERIKLREDNHEWTLLTYKHKQTKKDTKCVLFGWILAYYFFKKKIS
TSPPRDGGYFLSSSGRATTNELKEGERHLVSKLYTDDMRPETVTTYTTAQETKRKIS
TSPPRDGGYFLSSSGRATTNELKEGERHLVSKLYTDDMRPETVTTYTTAQETKRKIS
QTKKEVSIKTTLKELVHKRVTSPEDWMMQPDSYIEMMAQPGGENLLKNTLEICTLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARTKYAPEDLILEKABETSKLTNFSLPDTRTCRIFAFHGWNYVKVCHAICCVLNRQGGKR
NTVLFHGPASTGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEBAGNFGQ
QVNQFYAICSCQAIRIDQKGKGSKQIEPTPVIMTNBNITYNRIGCERPEHTQPIRD
RMLNIHITHTHGGDGLVDKNEWPHICAMLVKNGYQSTWASYCAKWGKVPDWSENWAE
PKVPPPINLLGSARSPFTPKGTPLSQNYALTPLASDLEDLALBEWSTPNTPVAGTAE
TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRL 10-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                 ö
                                                                                                                                                                                                                                                                                                                                         PAT 30-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parvovirus ns1 variants
Patent: BP 1077260-A 16 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
                                                                                                                                                               841 GAAGTITCTATITAAAACTACACTITAAAGAGCTGCATAAAAGAGTAACCTCACCACCAGAG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAAGTIGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGGTAACCTCACCAGAG 60
                                                                                                                          1 GAAGTIGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAMVM2 10-FEB-19: S081 bp DNA linear VRL 10\text{-}\text{FEB-}19: Minute virus of mice with two major open reading frames (genome).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coat protein; genome; origin of replication; overlapping genes; terminal repeat. Mice minute virus Mice minute virus Mice minute virus Viruses; sBONA viruses; Parvovirinae; Parvovirus. 1 (bases 1 to 5081)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mice minute virus
Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                 ö
Score 58.4; DB 6; Length 2019;
Pred. No. 2.7e-09;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.3%; Score 58.4; DB 6; Length 2019; Best Local Similarity 98.3%; Pred. No. 2.7e-09; Matches 59; Conservative 0; Mismatches 1; Indels 0.
                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Parvovirus NS1 variant"
1. .2019
/note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .2019
/organism="Mice minute virus"
/mol_type="unassigned DNA"
/db_xref="taxon:10794"
                                                                                                                                                                                                                                                                                                                            Sequence 16 from Patent BP1077260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nueesch, J. and Rommelaere, J.
                                                                                                                                                                                                                                                                                                                                                                                                                             AX137751.1 GI:14273925
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      97.3%;
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V01115.1 GI:60911
                                                                 59; Conservative
                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
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Thu Jun

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/ procefin_id="CAA24309.1"

/ db_xref="G1:60912"

/ db_xref="G0A:09134"

/ db_xref="G0A:PROJ134"

/ db_xref="G0A:PROJ134"

/ db_xref="G0A:PROJ134"

/ db_xref="GNA:PROJ134"

/ db_xref="GNA:PROJ144"

/ db_xref="GNA:PROJ144"
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STGKSIIAQAIAQAVGNVGCYNAANNNFPFNUCTNKNLIMVEEAGNFGQQVNQFKAIC
SGQTIRIDQKGKGSKQIEPTVVIMTYNENITVVRIGGEERFPHTQPIBRDRMLNIHLTH
TLPGALDDKUMMPPNICAMLYKGGYSTMASYCAKWGKVPDWSENWAEPKVPTPINL
IGSARSPFTTFKSTFLEKSTPLASHPLASDLEDLALEPWSTPNTPVAGTABTQNTGEAGS
KACQDGQLSPTWSEIEEDLRACFGABPLKKDFSBPLNLD"
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CRIRVHNTTDTSVKGNMAKDDAHEQIWTPWSLVDANAMGWHLQPSDWQYICNTMSQLN
LVSLDQEITANVLKTYTEQDLGGQAIKIYNNDLTACMWVANDNNILLEYTPAANSMET
LGFYPWKFTIASYTYTEQGGGAIKYYTENDGGTATRHYMGTPKGIPQFFTIENTQQI
TLLATGDEPATGTYYYYFDTNSVKLTHYMQTNRQLGQPPLLSTFPBADTDAGTLITAQGSHGTTQWGWNVSEAIRTRPAQVGFCQPHNDFBASRAGPFAADTTAGGSTLATAAGSSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="unnamed protein product; Protein sequence is in conflict with the conceptual translation; coding sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="NHLVLGWVPPGYKYLGPCNSLDQGEPTNPSDAAAKEHDBAYDQY
IKSGKNPYLYFSAADQRFIDQTKDAKDWGGKVGHYFFRTKRAFAPKLATDSEPGTSGV
SRAGKRTRPPAYIFINQARAKKKLTSSAAQQSSQTMSDGTSQPDSGNAVHSAARVERA
                                                                                                                                                                                                                                                                                                                                                                                 is spliced, but the exact splice sites are not known. The listed strand is complementary to the one which is included in the virion.
                                                                                                                                                                                                                                                                                                                           The messenger RNA of this virus (colinear with the strand listed)
Astell, C.R., Thomson, M., Merchlinsky, M. and Ward, D.C.
The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2286. .2154
/note="unnamed protein product; coding sequence"
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db_xref="GQ1:60913"

db_xref="GQA:P03137"

db_xref="SALSS-PROT:P03137"

/translation="MAPPAKRAKRGKGLRDGWLVGY"
                                                                                                                                                             Nucleic Acids Res. 11 (4), 999-1018 (1983)

    .5081
    /organism="Mice minute virus"

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/translation="MVGWWGINV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _xref="GOA:Q84207"
_xref="SPTREMBL:Q84207"
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/db_xref="G1:60914"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/db_xref="taxon:10794"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="GI:1335397"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                  parvovirus
                                                                                                                                                                                                                    83143341
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                                                                                                                                                                                                                    MEDLINE
PUBMED
                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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                                                                                                                                                                                                                                                                                                                           COMMENT
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Unging Source takes in the control of mice (Strain Markey); processing mouse I (variant A.9) cells.

The parvoviridae family cantains two groups that infect mammalian hosts: (i) defective (helper-dependent) adeno-associated viriuses, and (ii) autonomous (helper-independent) parvoviruses. MVM is a member of the latter group. Both groups have been demonstrated to package both plus and minus strands (in separate particles) of the ss. DNA genome, though the minus strand is more typically packaged in the latter group.

The sequence below corresponds to the plus (+) strand, also referred to as the C-strand. The minus (-) strand is also referred to as the V-strand.

The 3' and 5' termini both exhibit the potential for forming stable 'fold-back' hairpins; these sequences appear to play a role in
SVRYSYGKQHGENWASHGPAPERYTWDETSFGSGRDTKDGFIQSAPLVVPPPLNGILI
NANP IGTKONDIHESNVFNSYGPLTAFSHBSPYYYDGQLWDKELDLEHKRRLHITARFY
CKNNAPGQMLVRLGPNIJDQYDPNGATLSRIYTYYGTFFWKGKLTMRAKLRANTTWNPV
YQVSABDNGNSYMSVTKWLPPATGNQSVPLITRPVARNTY"
                                                                                                                                                                                                                                                                                                                           1101 GAAGTTTCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGGGTAACCTCACCAGGG 1160
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRL 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replication [1].
The left and right halves of the genome encode two distinct, but overlapping transcriptional units. The transcripts can be summarized [1] (1 map unit (mu) = 51 bp):
R1 (4.8 kb): 4.5 mu - 46 mu; 46+ mu - 95 mu
R2 (3.3 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu
R3 (3.0 kb): 40 mu - 46 mu; 46+ mu - 95 mu
R3 is the major transcript.
R3 is the wajor open anding frames, both on the plus (or C) There are two majors open reading frames, both on the plus (or C) strand. The left side ORF (261-2279) probably encodes a non-capsid protein of 85 kd; the right side ORF probably encodes the viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Three splicing patterns are used to excise the small intron common to all minute virus of mice RNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3783817 Original source text: Minute virus of mice (strain MVM(p)), passed
                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 5149)
Satell,C.K., Gardiner,E.M. and Tattersall,P.
DNA sequence of the lymphotropic variant of minute virus of mice,
MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Astell, C.R., Thomson, M., Merchlinsky, M. and Ward, D.C.
The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (bases 1 to 5149)
                                                                                                                                                                                                                                                                                             1 GAAGTIGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGAG
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                    ö
                                                                                                                                                                            Length 5081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J02275 M12520 M12521 M14704
J02275.1 GI:332293
alternative splicing; capsid protein; complete genome;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 11 (4), 999-1018 (1983)
                                                                                                                                                                            Score 58.4; DB 14
Pred. No. 2.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5149 bp ss-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVMPCG 5149 bp ss-DNA Minute virus of mice, complete genome.
                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prototype strain
J. Virol. 57 (2), 656-669 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morgan, W.R. and Ward, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nonstructural protein.
                                                                                                                                                                   97.3%;
                                                                                                                                                                                                                                    59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mice minute virus
Mice minute virus
                                                                                                                                                                                                    Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parvovirus
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                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
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MEDLINE
PUBMED
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TITLE
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                                                                                                                   DRIGIN
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GTSGVSRAGKRTRPPAYI FINQARAKKKLTSSAAQQSSQTMSDGTSQPDSGNAVHSAA
RVERAADGPGGSGGGGGGGGGVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMP
KSENYCRIRVHNTTDTSVKGNMAKDDAHEQIWTPWSLVDANAMGVWLQPSDWQYICNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSYDNOTHYR FLGDGWYEI TALATRL VHLIMPKSENY CRIRVHNTTDTS VKGNMAKDD
AHEQI WTPWSLVDANAWGVWLQPSDWQY I CNTMSQLNL VSLDQEI FNVVLKTVTEQDL
GGQAI KI YNNDLTACMMVAVDSINI ILPYTPAANSMETLGFY PWKPTIAS PYRYY YFCVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVGFCQPHNDFBASRAGPFAAPKVPADITYGVUALANNOONALOONALDERNTENNFNSY
PERYTWDETGFGSGROTKDGFLQSAPLVVPPPELNGILTNANPTGTKNDTHFSNVFNSY
GPLTAFSHPSPVYPQGQIWDKELDLEHKPRLHITAPFVCKNNAPGQMLVRLGPNLTDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSQLALJVSLDQETFUVVLKTVTEQDLGGQÄTKTYNNDLTACMMVAVDŠNNILPPYTPAA
NSMETLGFYPWKPTTASPYRYYFCVDRDLSVTYENQEGTVEHNVMGTPKGMNSQFFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENTQQITLLRTGDEFATGTYYFDTNSVKLTHTWQTNRQLGQPPLLSTFPEADTDAGTL
TAQGSRHGTTQMGVNWVSEAIRTRPAQVGFCQPHNDFEASRAGPFAAPKVPADITQGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKEANGSVRYSGRQHGENWASHGPAPERYTWDETSFGSGRDTKDGFIQSAPLVVPPP
LINGILINANDIGTKNDIHFSNVFNSGOELARENBSPYYGOGVWDKRELDLEHKPRLH
LINAFVCKNNAPGOMLYRLGPULTDOYDPNGATLSRIVTYGTFFWKGKLTWRAKLRAN
TTWNPVYQVSAEDNGNSYMSVTKWLPTATGNMOSVPLITRPVARNIY"
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QVGFCQPHNDFEASRAGPFAAPKVPADITQGVDKEANGSVRYSYGKQHGENWASHGPA
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AYDQYIKSGKNPYLYFSAADQRFIDQTKDAKDWGGKVGHYFFRTKRAFAPKLATDSEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MSDGTSQPDSGNAVHSAARVERAADGPGGSGGGGGGGGGVGVST"
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codon start=1

/product="unknown protein"

protein id="AAA67110.1"

/b xref="G1:825482"

/translation="MAPPAKRAKRGKGLRDGWLVGY"
                                                                                                           /note="alternative intron"
join(2286. .2316,2399. .4557)
/gene="VP1"
join(2286. .2316,2399. .4557)
/gene="VP1"
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2399. .>4557
/gene="VP1"
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/db_xref="GI:825484"
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/db_xref="GI:332296"
                                                                                                                                                                                                                                                                          /proteIn_id="AAA67111.1"
/db_xref="GI:332294"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MVGWWGINV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="ORF2; putative"
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/gene="VP"
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/gene="VP"
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/gene="VP"
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/gene="VP1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trafilation="MISGSGSINQGAKRKWAWFKVYKQLLKSVTYLFPHSVSRDAQKB
SNOLTMAGNAYSDBYLGATWALKEKSNQEVFSFYFKNENVQLAGKDIGWBYKKELGE
DELKSLQGRGAETTWDQSEDMEWETTVDENTKKVOYFIFDSLYKKCLFEVLAYTKNIFRGD
VNWFVQHEWGSDQGAHTCHVILGSKDFSQAGSWWRRQLAVYMSRWIYTACNVQLTPAB
RIKLREIAEDNEWYTLLTYKHKQTKKDYTKCYLFGNMIAYYFLTKKKISTSPPRDGGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MAGNAYSDEVLGATNWLKEKSNQEVFSFVFKNENVQLNGKDIGW
YSKKELQDEDELKSLQRGAETTWDGSEDMEWETTVDEMTKKQVFIFDSLVKKLLFBVL
NTKNI FPGDVNWFVQHEWGEDGGWHGHVLJGGKDFSQAQGKWWRRQLNVYWSFWLVTA
CNVQLTPABEI KLAETAEDMEWYTLLTYKHKQTKKDYTKCVLFGNMTAYYFLTKKKIS
TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRI
capsid proteins, VPI (or A, 83 kd), VP2 (or B, 64 kd), and VP3 (or C, 61 kd). But because of uncertainties about the precise splice points in the transcripts, the exact starts, stops and (possible) intron boundaries are not known.

revision 4804 4870 a-65bp-a in [2]; aa in [1] [2]
[3] sites; splice RIFFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRIQTKKEVSIK
TTLKELVHKRVTSPEDWMMQPDSYIEMMAQPGGENLLKNTLEICTLTLARTKTAFDL
ILEKAETSKLTNFSLPDTRTCRIFAFHGMNYVKVCHAICCVLNRQGGKRNTVLFHGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STGKSIIAQAIAQAVGNVGCYNAANVNPPFNDCTNKNLIWVEEAGNFGQOVNQFKAIC
SGQTIRIDQKGKGSKQIEPTPVIMTNNENITVVRIGCEERPEHTQPIRDRMLNIHLTH
TLPGDFGLVDKNEWPMICAMLVKNGYQSTWASYCAKWGKVPDWSENWAEPKVPTPINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QTKKEVSIKTTLKELVHKRVTSPEDMMMQPDSYIEMMAQPGGENLLKNTLEICTLTL
ARTKTAFDLILEKAETSKLTNFSLPDTRTCRIFAFHGMNYVKVCHAICCVLNRQGGKR
NTVLFHGPASTGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEBAGNFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVNQFKAICSGQTIRIDÕKGKĞSKÖIEPTPVIMTTNENITVVRIGCEERPEHTQPIRD
MRINIHLTHILGSGRGLYDVREWPHICHQMLVXRQYQSTWASVOKWGKVPDWSENWAE
PKVPTPINILGSARSPFTTPKSTPLSQNYALTPLASDLABDLALEPWSTPNTPVAGTAE
TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEFLKKDFSEPLNLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
KACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10794"
|lab_host="mouse | (variant A-9) cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="major transcription start site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product="nonstructural protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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/db_xref="GI:332295"
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/db_xref="GI:825481"
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/strain="MVM(p)"
                                                                                                                                                                                                                    sites; splice sites.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="putative"
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/gene="VP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        114. .2279
/gene="NS1"
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/gene="VP"
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/gene="VP"
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/gene="NS1"
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/gene="NS1"
                                                                                                                                                                                                                                                                    1. .5149
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NNYKKELQEDELKSLQRGAETTWDQSEDMEWESTVDEMTKKQVF1YDSLVKKCLFEVL
STKN1APADVTWFVQHEWGKDQGWHCHVL1GGKDFSQAQGKWWRRQLNVYWSRWLVTA
CNVQLTPAER1KLRE1AEDSEWVTLLTYKHKQTKKDYTKCVLFGNM1AYYFLTKKKIS
                                                                                                                                                                                                                                                                                                                                                                                                  OVNOFKAI CSGQTIRI DÖKGKĞSKQI EPTPVIMTTNENI TVVKI GCEERPEHTOPIRD
RMLNIHLTHTL PGDFGLVDKNEWPMI CAMLVKNGYQSTWASYCAKWGKVPDWTENWAE
PKVPTPINSLGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAE
                                                                                                                                                                                                                                                                                                              TSPENGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTALFLIKKREN
QTKKEVSIKTTLKELVHKRYTSPEDMMMQPDSYIEMMAQPGGENLLKNYLEICTLTL
ARTKTAFDLILEKAETSKLTNFSLPDTRTCKIFAFHGMNYIKVCHAICCVLNRQGGKR
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/mol type="egenomic DNA"
/mol type="egenomic DNA"
/db Zref="taxon:35340"
/clone="pRVXB36; pLTB/R13-6; pRTBg/H3-1"
265. .2283
265. .2283
                                                                                                                                                                                  /product="nonstructural protein 1"
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                                                                                                                                           gene="NS1"
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                                                                                                                                                                                                                                                                                                                                Viruses; Barvoviruses; Parvoviridae; Parvovirus.

1 (bases 1 to 4764)

Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses
J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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(bases 1 to 5144)

Ball-Goodrich, L.J. and Johnson, E.

Molecular characterization of a newly recognized mouse parvovirus

J. Virol. 68 (10), 6476-6486 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Besselsen, D.G.
Direct Submission
Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pathology, University of Missouri-Columbia, W213
Veterinary Medicine Bullding, Columbia, MO 65211, USA
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    Best Local Similarity 98.3%; Pred. No. 2.4e-09; Matches 59; Conservative 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /moi_type="genomic_DNA"
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/db_xref="taxon:42841"
                                                                                                                                                                                                         DNA
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Ball-Goodrich, L.J.
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Mouse parvovirus 1b
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Mouse parvovirus 1
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MSHVNLHSLDQELENVVIKTYTEQNTGAEÄVKIYNNDLTASMYVALDENNILPYTPAT
DNOETLGFYPWKPTMPSPYRYYFNCDRSLSVTYTDQTGSIVDTMANASGLSSQFFTIE
NTQRIQLLRTGDEFATGTYYFETEPIKLSHTWQSNRQLGQPPQITDLPTADNENATLV
                                                                                                                                                                                                                                                                                                                                                            GTSGYSIAGKRTKPPAHIPINQARAKKKRASLAAQQRTQTMSDGAEQPDSGSAVQSAA
RVERAADGPGGSGGGGGGGGGVGVSTGSYDNQTHYRPLSDGWVEITAYSTRMVHLNMP
KSENYCRVRVHNTNDTRTAGNMAKDDAHEQIWTPWSLIDSNAMGVWFQPSDWQFICNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAPFVCKNNAPGQLLVRLÄPNLTDQYDPNSSTLSRIVTYĞTFFWKGKLTLKAKLRPNA
TWNPVYQVSAQYQNENEYMSIHKWLPTATGNMQSIPLLSRPVARNTY"
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                                                                                                                                                                                                                                                                                           /trānslation="MAPPAKRAKRGWVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDE
AYDKYIKSGKNPYLYFSAADQRFIDQTKDAKDWGGKVGHYFFRTKRAFAPRLASSSEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRGDRSGITQISGSNDVTEATRVRPAQVGFCQPHDNFETSRAGPFKVPVVPANVTQGN
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NNILTNSDPIGNKTAIHYQNVFNSYGPLTAFPHPAPIYPGGIWDKELDLEHKPRLHA
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Molecular characterization of newly recognized rodent parvoviruses J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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Viruses; sebNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

1 (bases 1 to 4761)

1 (bases 1 to 4761)
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rontgeagskacodgolsptwseleedlracfgaeplkkofseplnld"
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90.3%; Score 54.2; DB 14; Length 5144;
Best Local Similarity 94.9%; Pred. No. 6.4e-08;
Matches 56; Conservative 0; Mismatches 3; Indels 0;
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                    join(2290. .2320,2403. .4561)
                                                                    Join(2290, .2320,2403. .4561)
/gene="VP1"
                                                                                                                                                                                           /product="capsid protein"
/protein_id="AAA61406.1"
/db_xref="GI:525327"
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KACQDGQLSPTWSEI EEDLRACFGAEPLKRDFSEPLNLD"
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                                                                                                                                                                             protein_id="AAA69567.1"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="ORF1; putative"
/codon_start=1
                                                /gene="NS1"
/product="NS-1 mRNA"
                                                                                                                                                                                                 db xref="GI:332291"
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/gene="VP"
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/gene="VP"
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/gene="VP1"
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/gene="VP"
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/gene="VP1"
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SNOLTWAGNAYSDEVIGTTNWIKEKSNOEVFSFVFKTEDVQINGKDIGWNNYKKELOE
DELKSLORGAETTWDOSEDMEWESTVDEMTKKOVFIYDSLVKKCLFEVISTKNIAPAD
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RIKLREIAEDSEWVTLLTYKHKQTKKDYTKCVLFGNMIAYYFLTKKKISTSPPRDGGY
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TLPGDFGLVDKNEWPMICAMLVKNGYQSTMASYCAKWGKVPDWSENWAEPKVPTPINS
LGSARSPFTTPKSTPLSQNYAITPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
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ILEKAETSKLTNFSLPDTRTCKIFAFHGMNYVKVCHAICCVLNRQGGKRNTVLFHGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Astell, C.R., Gardiner, E.M. and Tattersall, P.
DNA sequence of the lymphotropic variant of minute virus of mice,
MVM(1), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                               1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAAACCTCACCAGA 59
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1 (bases 1 to 5085)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minute virus of mice (MVM(i)), a lymphotropic variant of MVM
                                     Direct Submission
Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pathology, University of Missouri-Columbia, W213
Veterinary Medicine Building, Columbia, MO 65211, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                        Query Match 87.7%; Score 52.6; DB 14; Length 4761; Best Local Similarity 93.2%; Pred. No. 2.2e-07; Matches 55; Conservative 0; Mismatches 4; Indels 0;
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                                                                                                                                                                                          /mol_type="genomic DNA"
|strain="Cutter"
| specific host="Mesocricetus auratus"
|db_xrefe"taxon:10794"
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/clone="pBG222"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5085 bp ss-DNA
                                                                                                                                                                        organism="Mice minute virus"
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J. Virol. 570, 656-669 (1986)
86115415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115. .2280
/gene="NS1"
2 (bases 1 to 4761)
Besselsen, D.G.
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/gene="NS1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome.
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                                            TITLE
JOURNAL
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MVMICG
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VERSION
KEYWORDS
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TITLE
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MEDLINE
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                      AUTHORS
    REFERENCE
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/ LTAIN 1 AL 10AB. "MAGNAY SDEVLGTTNWILKEKSNOEVFS FV FKTEDVOLNGKDIGW
NNYKKELQEDELKSLORGAETTWDOSEDMEWESTVDEMTKKOVFI VDSLUKKCLFEVL
STRIA JAPDAVEVOHEWGRADGEWHCHLIGGGEDSOAGGEWRRROLNVYWSRWLTA
CNVOLTPARSI KLIETAEDSEWYTLLTYKHKOTKKOYTKKVLFGWANTAY FELTKKKIS
TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETVYTTAQETKRKRIS
TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETVYTTAQETKRKRIS
TSPRRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETVYTTAQETKRGRI
TAKTAFDLILEKAATSKLTHNSLEDPTRTKTI FAFHGWNYVKVCHAICCVLNRQGGKR
NTVLEHGEDASTGKSTI TAQAIAQAVGNYGCYNAANVNPFFNDCTNKNILWYERAGNFG
OVNOFKAICSGQTIRIDQKGKGSKQIEPTFVIMTTNENITVYRIGGERFEHTQPIRD
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AYDQYIKSGKNPYLYFSAADQRFIDQTKDAKUMGGKYGHYFFRTKRAFAPKLATDSEP
GTSGVSRAGKRTRPPAVIFINOARAKKATISSAAQOSSQTMSDGTSOPDGGNAVLADA
RVERAADGPGGSGGGGGGGGGYGGYGTKSYNQTHYR FLADGWVEITALATRLYHLNMP
KSENYCRIRVHNTTDTSVKGNNAKDDHEQIMTPWSLUDANAMGWLQPSDWQYICNT
MSQLNIVSLDQEIFNYVLKTYTEQDSGGQAIKIYNNDLTACMWYAUDSNNILPYTPAA
NSMETLGFYWKPTIASPYRY FKVDRDSLSYTYENDGGTIEHWYMGTPKGMNSQFTI
BNYQQITLLRYDGBTATGTY FPONDENSYTYENGGTIEHWYMGTPKGMNSQFTI
TAQGSRHGATQMYSTATGTPSPROWGFCQPHNDFRASRAGPFAAPKVPADVTQGV
DREANGSYRYSYGKQHGENWAAHGPAPERYTTWDETNEGSGRPTRDGTIGSAPLVVPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RMINIHLTHTLFGDFGLVDKNEWPMICAWIVKNGYQSTWASYCAKWGKVPDWSENWAE
PKVPTPINSLGSARSPFTTPKSTPLSQNYAITPLASDLEDLALEPWSTPNTPVAGTAE
TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPIKRDFSEPINLD"
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ITAPPVCKNNAPGQMLVRLGPNLTDQYDPNGATLSRI VTYGTFFWKGKLTMRAKLRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTWNPVYQVSVEDNGNSYMSVTKWLPTATGNMQSVPLITRPVARNTY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003. .4558
/gene="VP"
2003. .2281
/gene="VP"
/note="major transcription start site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="minor transcription start site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2007. .2281
|gene="VP"
|note="minor transcription start site"
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/db_xref="G1:825478"
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protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="alternative intron"
join(2287. .2317,2400. .4558)
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join(2287. .2317,2400. .4558)
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I ENVULKTYTEQDSGGQAIK YNNDLTACMMANDSNNILBYTPAANSMETIGFYPWK
PTIASPYRYYFCVDROLSYTYENQEGTIEHNVMGTPKGMNSQFFTIENTQQITLLRTG
DEFATGTYTPTAPQTNRCINGULGOPPLLISTPERADTOGTLTAGGSRHGATQM
EVNMVSEAIRTRPAQVGFCDHNDFRASRAGPFAAPKVPADVTGGVDREANGSVRYSY
GKQHGENWAAHGPRYTWDETHFOSGRDTRDGFTQSAPLVVPPPLNGILTNANDIG
TKNDLHFSNVFNSYGPELTAFSHPSPYYPQGQIWDKELDLEHKPRLHITAPFVCKNNAP
GQMLVRLGPNLTDQYDDNGATLSRIVTYGFFWKGKLLTMRAKLRANTTWNPYYQVSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGILTNANNPIGTRNDIHESNVFNS
YGPLTAFSHPSPVYPOGQIMDKELDLEHKPELHITAPFVCKNNAPGGMLVRLGFBNVFND
QYDPNGATLSRIVTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKWL
PTATGNMQSVPLITRPVARNTY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPPAYIFINOARAKKKLTSSAAQOSSOTMSDGTSQPDGGNGVHSAARVERAADGPGGS
GGGGSGGGGGVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCRIRVHN
TTDTSVKGNMAKDDAHEQIWTPWSLVDANAMGVWLQPSDWQYICNTMSQLNLVSLDQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRDLSVTYENQEGTIEHNVMGTPKGMNSQFFTIENTQQITLLRTGDEFATGTYYFDTN
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AQVGFCQPHNDFEASRAGPPAAPKVPADVTQGVDREANGSVRYSYGKQHGENWAAHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="VPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDEAYDQYIKSGKNP"
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Data kindly reviewed (18-JUL-1986) by G. McMaster.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNGNSYMSVTKWLPTATGNMQSVPLITRPVARNTY"
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93.2%; Pred. No. 2.2e-07;
ive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="terminal hairpin region"
                                                                                                                                                                   note="terminal hairpin region"
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/note="polyadenylation signal"
4878. .5087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="polyadenylation signal"
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/db_xref="GOA.P07302"
                                                            /organism="Mice minute virus"
/mol_type="genomic DNA"
/db_xref="taxon:10794"
1. 7116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="VP2 protein"
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/db xref="G3:541907302"
/db xref="G0A:P07302"
/db_xref="SWISS-PROT:P07302"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      function="coat protein"
                                                                                                                                                                                                                                                                                                                                      unction="coat protein'
                                                                                                                                                                                              .76. .183
'note="TATA box"
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                                                                                                                                                                                                                                                                                      <2405. .4558
/gene="VP1"
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/gene="VP2"
<2792. .4558
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/gene="VP1"
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Best Local Similarity 93.2
Matches 55; Conservative
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                        FEATURES
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DNA sequence comparison between two tissue-specific variants of the
autonomous parvovirus, minute virus of mice
Nucleic Acids Res. 13 (10), 3617-3633 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PANVMI 5087 bp DNA linear VRL 01-JUL-1999 Mouse parvovirus minute virus immunosuppressive variant genome ( =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSDGTSQPDGGNAVHSAARVERAADGPGGSGGGGGGGGGVGVSTGSYDNGTHYRFLGDGWYEITALATRLVHLNMFKSENYCRIVHYNHYTDTGYKGNNAKDD AHEQIWFPWARSUVDANAWGVYLGYBNSQLNLVSLDQEIFWVLKTVTEQDSGGQAIKIYNNDLTAGAWVAVDSNNILEYTPAANSMETLGFYPWRETIASBYRKYFCVD RDLSVTYENQGGTIEHNVMGTPKGMNSQFFTIENTQQITLLKTGDEFATGTXYFDTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVGFCOPHNIPEASRACPFAAPKVPADVTQGVDREANGSVRYSYGKQHGENWAAHGPA
PERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGILTNANPIGTKNDIHFSNVFNSY
GPLTAFSHPSPVYPQGQIWDKELDLEHKPRLHITAPFVCKNNAPGQMLVRLGPNLTDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATQMEVNWVSEAIRTRPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YDPNGATLSRIVTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKWLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coat protein; genome; origin of replication; overlapping genes; terminal repeat; unidentified reading frame.
Mice minute virus
Mice minute virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1. (bases 1 to 5087)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MFNYLFYRPEITWF"
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db_xref="GI:825480"
                                                          'note="alternative intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /proteIn_id="AAA69572.1"
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                                                                                                                                                                                                                                               'translation="MVGWWGINV"
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                                                                                                                                                                                                                                                                                                                     /note="ORF2; putative"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
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/gene="VP1"
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/gene="VP2"
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/gene="VP1"
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/gene="VP2"
                                                                                .2362
                                                                                                      gene="VP1
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Matches 5
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TITLE
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VRL 21-AUG-1996
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Hamster parvovirus
Viruses; Barvoviridae; Parvovirinae; Parvovirus.
Viruses; BaDN viruses; Parvoviridae; Parvovirus.
1 (bases 1 to 4773)
Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses
J. Gen. Virol. 77 (Pt. 5), 899-911 (1996)
                                                                                                                                            Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

(bases 1 to 4764)
Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses
J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pathology, University of Missouri-Columbia, W213
Veterinary Medicine Building, Columbia, MO 65211, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           Submitted (17-AUG-1995) David G. Besselsen, Department of Veterinary Pathology, University of Missouri-Columbia, W213 Veterinary Medicine Building, Columbia, MO 65211, USA Location/Qualifiers
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/organism="Hamster parvovirus"
/mol_type="genomic DNA"
/apecific host="Mesocricetus auratus"
/db_xref="taxon:42843"
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|mol_type="genomic DNR"
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desselsen, D.G.
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Besselsen, D.G.
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Mouse parvovirus 1c
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AAV52148 Streptoco
ABX08031 S. pneumo
ABX50132 Bovine ES
AAX30921 Streptoco

AAD02798 standard; DNA; 60 BP.

AAD02798;

/\*tag= b /note= "This location corresponds to position 847 of the NS1 variant (5283A) DNA shown in AAD02799" Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity. NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds. Parvovirus non-structure protein 1 (NS1) variant (S283A) DNA fragment. /product= "Parvovirus NSI variant (S283A) peptide" /note= "CDS does not include start and stop codon" (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM. Location/Qualifiers replace (7, A) 99EP-00115161 99EP-00115161 (first entry) ø /partial 1. .60 /\*tag= Rommelaere (revised) WPI; 2001-212717/22. P-PSDB; AAY72703 EP1077260-A1 13-AUG-1999; 13-AUG-1999; 06-AUG-2003 31-MAY-2001 21-FEB-2001 Parvovirus. Synthetic. Nueesch J, mutation Key THE STATE OF THE S

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therapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                The present sequence is a parvovirus non-structure protein 1 (NS1) variant ($283A) DNA fragment. The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-NUG-2003 to correct OS field.)
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/product= "NS1 variant (S283A) protein"
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               Disclosure; Page 11; 41pp; English
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/product= "NS1 variant (T363A) protein"
replace(1187, A)
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                                                                                                                      60; Conservative
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                                                   Query Match
Best Local Similarity
Matches 60; Conserv
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The present sequence is a DNA encoding parvovirus non-structure protein 1 (NS1) variant (T394A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSI; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gené therapy; mutant; mutein; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; ds.
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                                                                       Parvovirus non-structure protein 1 (NS1) variant (T394A) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2019 BP; 697 A; 389 C; 453 G; 480 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                         /*tag= a
/product= "NS1 variant (T394A) protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58.4; DB 5;
Pred. No. 3.2e-11;
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1. .2019
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(first entry)
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(first entry)
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Best Local Similarity 98.3
Matches 59; Conservative
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                    06-AUG-2003
31-MAY-2001
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31-MAY-2001
                                                                                                                                                                Parvovirus
                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                                 mutation
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a DNA encoding parvovirus non-structure protein (NSI) variant (1463A). The invention relates to the variants of the parvovirus non-structure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytocoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-ANG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                          NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
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                                                                                                                                                                                                                                        Parvovirus non-structure protein 1 (NS1) variant (T463A) DNA.
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/product= "NS1 variant (T463A) protein"
replace(1387, A)
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1. .2019
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                                                                                                             BP
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                                                                                                                                                                                                        (first entry)
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P-PSDB; AAY72710.
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Best Local Similarity
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31-MAY-2001
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Parvovirus Synthetic

mutation

AAD02805;

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Gaps ö

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RESULT

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AAD02803

Length 2019;

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11116 GAAGTGTCAATCAAATGTACTTGCGGGACTTGGTTAGTAAAAGAGTAACATCACCTGA 1174
                                                                                                                                              This viral DNA is isolated from a non- attenuated CPV. The DNA is preferably derived from vB1440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pGEM3Z or pGEMSZ. The host cells to be transfected ar selected from Norden Laboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells or canine A72 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dog; vaccine; CPV; myocardial disease; enteric disease; ds;
                                                Attenuated CPV strains contg. up to 4 mutation (s) relative to control virus - useful as a veterinary vaccine against CPV disease in animals, such as wild or domestic dogs.
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0
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                                                                                                                                                                                                                                                                                                                               19; Indels
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                                                                                                                 Claim 1; Page 21-24; 42pp; English
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Best Local Similarity 67.8%;
Conservative
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structure protein 1 (NS1). The present invention relates to the variants
of the parvovirus non-structure protein (NS1) having a shifted
equilibrium between the DNA replication and transcription activities, and
the cytotoxicity activity. These variants are useful as toxins for
treating tumoural diseases. The variant DNAs are useful as vectors for
gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                  Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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Pred. No. 3.2e-11;
0; Mismatches 1; Indels 0:
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                                                                                "Parvovirus NS1 protein"
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                             Location/Qualifiers
1. .2019
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nes 59; Conservative
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P-PSDB; AAY72702.
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                                                                                                                                                 This viral DNA is isolated from an attenuated CPV. The DNA is preferably derived from vB1440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pd8732 or pGEM52. The host cells to be transfected ar selected from Norden Laboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells or
                                                                                                                                                                                                                                                                                                                                                                               /*tag= c
/note= "base 4307 is A in virulent CPV-39 (G in passage
65 attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "base 4973 is C in virulent CPV-39 (T in passage 65 attenuated virus)"
                                                                                                                                     1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= g
/note= "base 4889 is C in virulent CPV-39 (T in passage
65 attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                                                                                        note= "base 4358 is C in virulent CPV-39 (T in passage 55 attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in passage
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (A in
                                                                                                                                                                                                                                                                  parvovirus; CPV; attenuation; vaccine; dog; panleukopenia virus; mink enteritis virus; infection; ds.
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                                                                                   Sequence 5049 BP; 1790 A; 814 C; 1029 G; 1416 T; 0 U; 0 Other;
                                                                                                 th 47.7%; Score 28.6; DB 2; Length 5049; Similarity 67.8%; Pred. No. 2.4; 40; Conservative 0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= e
/note= "base 4409 is C in virulent CPV-39
65 attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= f
/note= "base 4477 is G in virulent CPV-39
65 attenuated virus)"
                                                                                                                                                                                                                                                                                                                              /*tag= a
/mote= "NS1/NS2 coding region"
                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/note= "VP1/VP2 coding region"
i307
                                                                                                                                                                                                                                                  Attenuated canine parvovirus genomic DNA.
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
         Claim 2; Page 24-27; 42pp; English.
                                                                                                                                                                                                BP
                                                                                                                                                                                                AAT88321 standard; DNA; 5049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US007584
                                                                                                                                                                                                                                                                                                                                              .4541
                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                   *tag=
                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                             parvovirus
                                                                  canine A72 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9742972-A1
                                                                                                                                                                                                                                  21-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-1997
                                                                                                                                                      1116
                                                                                                                                                                                                                  AAT88321;
                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation
                                                                                                                                                                                                                                                                                                                                                                                                         mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                           mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutation
                                                                                                                                                                                                                                                                    Canine
                                                                                                                                                                                                                                                                             Feline
                                                                                                                                                                                                                                                                                            Canine
                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                 - nsed as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Attenuated viruees are obtained by serial passage of the virulent CPV type 2b isolate 39 in NLFK feline kidney host cells. They have one or more of the sequence alterations indicated in the sequence relative to the sequence of a control (5th passage) wild-type CPV-2b (see AAT88320). A claimed virus from the 65th passage (deposited as ATCC W 2528) contains all 6 mutations. The DNA from attenuated CPV strains (see also AAT88324) is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks of the virus. The attenuated viruses can be used in dogs as a vaccine to protect against CPV disease, or more generally in cats and minks to protect against feline patheukopenia virus and mink enterettis virus. The variations where the virus and minks to the variation of the virus and minks to the variations and virus and minks to the variations and virus and minks to virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1116 GAAGTGTCAATCAATGTACTTTGCGGGACTTGGTTAGTAAAGAGTAACATCACCTGA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccines protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), providing a long term immune response. (NB. this sequence was created by adaptation of the wild-type CPV-2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This DNA molecule encodes an annenuated canine parvovirus (CPV) genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAAGTIGCTATTAAAACTACACTTAAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA
                                                                                                                                                                                                                                                canine parvovirus DNA carrying specific attenuating mutation(s) - use vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "base 97 is C or T in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parvovirus; CPV; attenuation; vBI440; vaccine; dog; panleukopenia virus; mink enteritis virus; infection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5049 BP; 1788 A; 809 C; 1029 G; 1417 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.7%; Score 28.6; DB 2; Length 5049; 67.8%; Pred. No. 2.4; o; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G in CPV-39 (passage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Attenuated canine parvovirus (vBI440) genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b
/note= "VP1/VP2 coding region"
4745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag= a
'note= "NS1/NS2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parvovirus; vBI440 (ATCC VR 2489).
                                                                                                                                      Carmichael LE, Gruenberg A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c
"base 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT88324 standard; DNA; 5049 BP
                                                                 CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 67.8%;
les 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence given in AAT88320)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ש
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
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                                                                                                                                                                                                            WPI; 1998-008583/01
15-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2003
21-MAY-1998
                                                                                                                                      Parrish CR,
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/note= "VP1/VP2 coding region"

/\*tag=

CDS

WO9742972-A1.

20-NOV-1997

Location/Qualifiers 273. .2279 /\*tag= a /note= "NS1/NS2 c 2286. .4541

Key

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This DNA sequence comprises an attenuated virus genome derived by serial passaging (60 times) of virulent canine parvovirus (CPV) type 2b isolate passaging (60 times) of virulent canine parvovirus (CPV) type 2b isolate 23 in NuEK feline kidney host cells. The attenuated virus is designated vB1440 (ATCC VR 2489). It contains 4 mutations relative to the sequence (see AAT88320) of the control (5th passage) wild-type CPV-2b. 2 mutations are within the hairpin formed by the 3' terminal palindrome: the mutation at nucleotide 59 introduces an A into a G-C rich region within the tip of the hairpin, disrupting the base pairing in one of the 2 small internal palindromes within that sequence; the thymine at nucleotide 97 is the mainstached bubble (flip-flop) sequence within the palindrome. The DNA from attenuated CPV strains (see also AAT88321) is used for the production of infectious molecular DNA clones, which, in the trun, can be transfected into cells to generate master stocks of the virus. The attenuated viruses can be used in dags as a vaccine to protect against feline panleukopenia virus and mink enteritis virus. The vaccines protect against the currently prevalent CPV-2b type (and all extant strants of types 2 and 2a), providing a long term immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                     Canine parvovirus DNA carrying specific attenuating mutation(8) - used as vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5049 BP; 1791 A; 812 C; 1029 G; 1417 T; 0 U; 0 Other;
/*tag= e
/note= "base 4745 is T in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.7%; Score 28.6; DB 2; Length 5049; 67.8%; Pred. No. 2.4;
                                                             /*tag= f
/note= "base 4881 is C in CPV-39 (passage
                                                                                                                                                                                                                                                                                                                                         Gruenberg A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Page 34-37; 60pp; English.
                                                                                                                                                                                                                                                                                               (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                             97WO-US007584,
                                                                                                                                                                                                                                                      96US-00647655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.8%;
                                                                                                                                                                                                                                                                                                                                         Carmichael LE,
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-008583/01
                                                                                                                                                                                                               06-MAY-1997;
                                                                                                                              WO9742972-A1
                                                                                                                                                                                                                                                                                                                                         Parrish CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                           mutation
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Canine parvovirus DNA carrying specific attenuating mutation(s) - used as vaccines for protection against parvovirus and feline pan-leukopenia

Example 8; Page 37-40; 60pp; English.

virus infections.

Carmichael LE, Gruenberg A;

WPI; 1998-008583/01.

Parrish CR,

(CORR ) CORNELL RES FOUND INC.

97WO-US007584. 96US-00647655.

36-MAY-1997; 15-MAY-1996;

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This DNA sequence comprises the genome of virulent canine parvovirus type 2b (CPV-2b) isolate 39, obtained after 5 serial passages in NLFK feline kidney host cells. Further passaging has yielded attenuated virus vBI440 (ATCC VR 2489) (see AAT88324) from the 66th passage, and a claimed virus (see AAT88321) derived from the 65th passage (ATCC 2528). These (see AAT88321) derived from the 65th passage (ATCC 2528). These passage virus. The DNA from attenuated CPV-2b strains is used for the passage virus. The DNA from attenuated CPV-2b strains is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks of the virus. The cattenuated viruses can be used in dogs as a vaccine to protect against cattenuated virus and mink enteritis virus. The vaccines protect against companially in cats and minks to protect against feline panleukopenia virus and mink enteritis virus. The vaccines protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), and provide a long term immune response. (Updated on 17-0003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1116 GAAGTGTCAATCAAATGTACTTTGCGGACTTGGTTAATAAAAGAGTAACATCACCTGA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAAGTIGCIATIAAAACTACACTIAAAGAGCIGGIGCAIAAAAAGAGIAACCICACCAGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5049 BP; 1789 A; 813 C; 1030 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 47.7%; Score 28.6; DB 2; Length 5049; Best Local Similarity 67.8%; Pred. No. 2.4; Matches 40; Conservative 0; Mismatches 19; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prokaryotic essential gene #9353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACA27696 standard; DNA; 2931 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug design; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense, ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACA27696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACA27696
BXBXBXBXBXBXBXBXB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    parvovirus; CPV; attenuation; vBI440; vaccine; dog; panleukopenia virus; mink enteritis virus; infection; ds.
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GAAGTGTCAATCAATGTACTTTGCGGGACTTGGTTAGTAAAAGAGTAACATCACCTGA 1174
                               1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA 59
          ;
0
         19; Indels
                                                                                                                                                                            Canine parvovirus 39 passage #5 (wild-type).
         0; Mismatches
                                                                                                     AAT88320 standard; DNA; 5049 BP
                                                                                                                                                         (first entry)
Local Similarity 67.8
nes 40; Conservative
                                                                                                                                              (revised)
                                                                                                                                              17-OCT-2003
21-MAY-1998
                                                                                                                           AAT88320;
   Best Loca
Matches
                                                                                   RESULT 11
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Canine parvovirus; type 2b isolate 39.

Canine Eeline Gene #2617 used to diagnose liver cancer.

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the invention relates to an isolated muciest acid compitising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or polypeptide whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide of its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular proliferation, or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway capable of proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiocic; (10) profiling a compound that inhibits proliferation of the test compound that inhibits proliferation of the strains is present in a culture or collection of the compound; a compound; so exemptions of the strains is present in a culture or collection of the strains is present in a culture or collection of the strains is present in a culture or collection of the strains in spressing the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for dentifying proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids actional corpusants or the screening homologous nucleic acids required for proliferation or or lessented molecules for rational corpusants or or objections or or or or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K. pneumoniae or P. aeruginosa. The present sequence is one of the margin prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed precipilation.
                                                                                                                                                                                                                                                                                                                                                                                                                                            screening
                                                                                                                                                                                                                                                                                  Zyskind JW;
Xu HH:
                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2931 BP; 1135 A; 299 C; 597 G; 900 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                  Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                  Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; SEQ ID NO 15566; 1766pp; English.
                                                                                                                                                                                                                                                                                  Malone C,
Carr GJ,
                                                                                               2001US-00948993.
2001US-0342923P.
2002US-00072851.
                                                                          2001US-00815242
                          21-MAR-2002; 2002WO-US009107
                                                                                                                                                                            2002US-0362699P
                                                                                                                                                                                                                               (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                  Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; ABU23826
                                                                                               06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                          21-MAR-2001;
                                                                                                                                                                               06-MAR-2002;
                                                                                                                                                                                                                                                                                  Wang L,
Wall D,
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                                Gaps
                               ö
                                                             48
                               13; Indels
                                                             2 AAGTIGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTA
                             0; Mismatches
 Score 26.2;
Pred. No. 16;
vuery match
Best Local Similarity 72.3%;
Matches 34; Conservative
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1091 AAGAAGTAGTTAAAAAAAACACTTAAAAGGCTTGTTAAAAATGGAATA 1137
                                                                      ABN96119 standard; DNA; 388
                                               RESULT 13
                                                         ABN96119
XX
XX
AC ABN9
XX
DT 13-A
   g
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(first entry)

13-AUG-2002 ABN96119;

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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN3503.ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, and positive, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form par of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAAGTIGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acetyl-coenzyme-A-carboxylase; acetyl-CoA-carboxylase; ACCase; transgenic plant; oilseed; crop improvement; fatty acid; polyhydroxyalkanoate; poly-beta-hydroxyalkanoate; herbicide resistance; pesticide resistance; polyhos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                             Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease st disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
42.3%; Score 25.4; DB 6; Length 388;
Best Local Similarity 64.4%; Pred. No. 20;
Matches 38; Conservative 0; Mismatches 21: Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 388 BP; 139 A; 68 C; 66 G; 115 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Vockley JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                       Peres-Da-Silva S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 2617; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis ACCase clone pKLU81.
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AAQ77691
XX
XX
AC AAQ77691 standard; cDNA; 565 BP
XX
C AAQ77691;
XX
DT 25-WAR-2003 (revised)
DT 08-WAY-1995 (first entry)
XX
XX
Actional Accase clone pKLU81
XX
XX
Actional Accase clone pKLU81
XX
XX
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                  02-OCT-2001; 2001WO-US030589.
                                                                                                                                                                                                                                                                                                                                            02-OCT-2000; 2000US-0237054P
                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                       Alvares C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-426119/45
                                                                                                                                                                                                       WO200229103-A2
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A cDNA clone of rapeseed, identified as encoding ACCase, was used to probe a genomic library prepared from A. thaliana. The 5' sequence of an isolated subclone, pKLU81, was determined. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                               /*tag= c
/note= "base n at position 526 is not identified in the
specification"
                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= d
/note= "base n at position 548 is not identified in the
specification"
556
                                                                                      tag= a
note= "base n at position 483 is not identified in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e
"base n at position 556 is not identified in the
                                                                                                                                                                                                                                            in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant DNA encoding acetyl coenzyme A carboxylase - used to transform plants to modify ACCase expression e.g. to increase poly:hydroxy-alkanoate prod. or herbicide resistance.
                                                                                                                                                                                                /*tag= b
/note= "base n at position 494 is not identified
specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 565 BP; 147 A; 98 C; 129 G; 186 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fentem PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Slabas A, Elborough KM, Bright SWJ,
                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 8; 47pp; English.
                                                                                                                                                     specification"
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                                                                                                                                                                                misc_difference
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                                                        misc difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
SOCCCCXXX PLANCE SEASON SEASON
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/\*tag= f /note= "unknown/unspecified residue"

/\*tag= e /note= "unknown/unspecified residue"

\*tag= c note= "unspecified/unknown residue"

note= "unspecified/unknown residue"

Arabidopsis thaliana; (clone pKLU81).

Location/Qualifiers

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\*tag= b ...268 \*tag=

misc\_feature

misc\_feature

\*tag= d note= "unknown/unspecified residue"

\*tag=

misc\_feature

misc feature

misc\_feature

WO9529246-A1 02-NOV-1995.

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The sequence represents the 5' end of subclone pKLUB1 (NCIB 40555)
cncoding the Arabidopsis thaliana acetyl Coenzyme A carboxylase (ACCase)
cncoding the Arabidopsis thaliana acetyl Coenzyme A carboxylase (ACCase)
cnbA, which can be used to create a sense or an antistense expression
cassette to transform rape and other oilseed plants (canola, soybean,
sunflower) to downregulate production of the ACCase enzyme. The
cransgenic plants have a lower or a modified oil content. Down-regulation
of oil synthesis can be used to divert the substrate, acetyl Coenzyme A,
into synthesis of alternative storage materials (starch, protein or novel
polymers e.g. polybydroxyalkanoates). Full-length ACCase clones can be
used to create transgenic plants over-expression in monocot plants such
as wheat, barley, maize and rice, which are normally sensitive to
herbicides resistance in the transgenic plants (dicocs are normally
cherbicide resistance in the transgenic plants (dicocs are normally
resistant to these herbicides). (Updated on 16-OCT-2003 to standardise OS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 565 BP; 147 A; 98 C; 129 G; 186 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Fig 8; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 68.6
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Gaps

; 0

16; Indels

0; Mismatches

Best Local Similarity 68.6 Matches 35; Conservative

TIGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCAC 55

406

g 8

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AAT04949 standard; cDNA; 565 BP

DNA encoding acetyl Coenzyme A carboxylase - used for developing plants with controlled expression of ACCase, e.g. for controlling fatty acid

synthesis.

Fentem PA

Slabas AR, Elborough KM, Bright SWJ,

(ZENE ) ZENECA LTD.

94WO-GB000846. 94WO-GB000846

21-APR-1994; 21-APR-1994; P-PSDB; AAR84623, AAR84622, AAR84624

WPI; 1995-382994/49

2, 2004, 19:08:26

Acetyl Coenzyme A carboxylase; ACCase; plasmid pKLU81; transgenic plant; modified oil content; polyhydroxyalkanoate polymer; herbicide resistance; monocot crop improvement; ss.

Arabidopsis thaliana acetyl-Coenzyme-A-carboxylase 5' sequence.

(first entry)

(revised)

16-OCT-2003 02-JUN-1996

RESULT 15
AAT04949/C
ID AAT04949/C
XX
AC AAT04
DT 16-OC
DT 02-JU
XX
XX
ACCET
XX
RW MODIF
KW MODOC

AAT04949;

Search completed: June Job time : 149.25 secs

Thu Jun 3 10:28:27 2004

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27.6 46.0 768 29 CNSOIV5E 27.4 45.7 562 28 BH068411 27.2 45.3 760 12 BJ438237 27 45.0 182 9 AV222962 27 45.0 282 9 AV15404 27 45.0 305 9 AV154012 27 45.0 427 13 BY453224 27 45.0 858 28 AZ684019	27 45.0 865 28 AZ687690 26.6 44.3 891 29 CNS03281 26.4 44.0 716 28 BZ973479 26.4 44.0 797 28 BZ973483 26.4 44.0 805 29 CG146849 26.4 44.0 916 28 CC358376 26.4 44.0 901 28 CC419705 26.2 43.7 423 13 BQ867043	26.2 43.7 506 28 AZ869268 26 43.3 205 13 BU352437 26 43.3 594 14 BU25629 26 43.3 634 13 BU480641 26 43.3 634 13 BU480641 26 43.3 652 13 BU304839 26 43.3 755 13 CA058415 26 43.3 755 13 BU34168 26 43.3 755 13 BU34168	C 35 26 43.3 771 12 BG180322 BG180322 602331171 B 26 43.3 771 12 BG180322 BG180322 602331171 B 26 43.3 771 29 BX222156 BD180 XE2 EXECUTES B 26 43.3 794 13 BU19292 BU19292 BU19292 603144628 BU19292 EXECUTES BU19292 EXECUTES BU19292 EXECUTES BU19292	ALIGNMENTS 117540 687 bp mRNA lir	Pectole - CAP VICIS VIDITERA CUNA C Bequence. CF517540. GI:34549308 CF517540.1 GI:34549308 EST. Vitis vinifera Vitis vinifera Eukaryota; Viridiplantae; Streptoph Spermatophyta; Magnoliophyta; eudic rosids; Vitaceae, Vitis.	AUTHORS Goes da Siva, F., Iandolino, A., Lim, H., Baek, J., Jones, K. and AUTHORS Cook, D.  TITLE Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages JOURNAL Unpublished (2003)  COMMENT CONTACT: Douglas Cook, PhD CAES Genome Pacility UC Davis, Plant Pathology One Shields Ave, Davis, CA 95616, USA Tel: 530 754 6561 Fax: 530 754 6617 Email: drcook@ucdavis.edu
GenCore version 5.1.6  Copyright (c) 1993 - 2004 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: June 2, 2004, 18:15:21; Search time 1499.5 Seconds (without alignments)	US-10-069-056-3 score: 60 : 1 gaagttgctattaaaactac table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 27513289 seqs, 14931090276 residues  Total number of hits satisfying chosen parameters: 55026578  Minimum DB seq length: 0  Maximum DB seq length: 2000000000  Post-processing: Minimum Match 00*  Maximum Match 100*  Listing first 45 summaries		12: gb_est3:* 13: gb_est4:* 14: gb_est5:* 15: em_estfun:* 16: em_estcm:* 17: em_gss_hum:* 18: em_gss_hum:* 19: em_gss_pln:* 20: em_gss_vrt:*	21: em_g8s_run:* 23: em_g8s_man:* 23: em_g8s_man:* 24: em_g8s_run:* 25: em_g8s_ron:* 26: em_g8s_ron:* 27: em_g8s_ron:* 27: em_g8s_ron:* 29: gb_g8s_1:* 29: gb_g8s_2:*	Score freeter than or equal to the score distribution.   Structured by analysis of the total score distribution.   SumWARIES

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/lab_host="DH5alpha"
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AZ246409/c
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VERSION
KEYWORDS
SOURCE
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                              Once-lorgan: Petiole; Vector: pDNR; Site 1: Sfil; Site 2: Sfil; CAP is a cDNA library of Vitis vinifera cv. Cabernet Sauvignon. Clone 8 petioles. Samples were collected on July 10, 2002 from plants on the onset of Veraison (berry softening). Sampled vines were located the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA12E1301IIR G12 Cabernet Sauvignon Leaf - CA12E1 Vitis vinifera cDNA clone CA12E1301IIR_G12 3', mRNA sequence.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, Vitaceae, Vitis.
                                                                                /mol_type="mRNA"
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/dev_stage="Onset of Veraison (berry softening)"
/lab_host="DH5alpha"
/clone lib="Vitis vinifera cv. cabernet sauvignon (Clone 8) Petiole - CAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
S'-ATTCTAGAGGCCGACGACATG-dT(130)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAAGTIGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA 59
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Goes da Silva, F., Lim, H., Iandolino, A., Baek, J., Jones, K.,
Walker, M.A. and Cook, D.R.
Transcriptional responses of Vitis vinifera to infection by the
bacterial pathogen Xylella fastidiosa
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.3%; Score 30.2; DB 14; Length 687; llarity 69.5%; Pred. No. 12; Conservative 0; Mismatches 18; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:29960"
/clone="CA12E13011IR_G12"
/sex="hermaphrodite"
/dev_stage="Mid-season leaf material"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UC Davis Department of Plant Pathology
1 Shields Ave., DAvis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
                                                              'organism="Vitis vinifera"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Vitis vinifera"
Seg primer: GCCAAACGAATGGTCTAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: GCCAAACGAATGGTCTAG.
                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cloning as follows
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CAES Genome Facility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vitis vinifera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches 4
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                  FEATURES
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/clone libe Cabernet Sauvignon Leaf - CA12EI"
/clone libe Cabernet Sauvignon Leaf; Vector: pDNR; Site 1: Sfil; Site 2:
Sfil; CA12EI is a cDNA library of Cabernet Sauvignon
leaves. The leaves were collected on July 25, 2001, in
Napa Valley, California, and represent leaves in
mid-season development. These leaves were verified to be
infected with the bacterial pathogen, Xylella fastidiosa,
based on a diagnostic assay using PCR and Xylella-specific
primer pairs. The plants were asymptomatic at the time of
collection, but later developed symptoms. CDNAs were made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AACCAGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
5'-AATCTAGAGGCGGGCGCACATGCGCCATTACGCCGGG-3' and
size-selected using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: schaoœtigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac.edu/mouse/bac_end_intro.html
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Mus musculus
Mus maculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 538)
Zhao, S., Nieman, W., Feldblyum, T., Malek, J., Shatsman, S.,
Akinret, B., Levins, M., Megann, S., Tsegaye, G., Geer, K., Krol, M., de
Mouse BAC End Sequences from Library RPCI-23
Opther_GSSS: RPCI-23-92L24.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 50.3%; Score 30.2; DB 14; Length 777; Best Local Similarity 69.5%; Pred. No. 12; Matches 41; Conservative 0; Mismatches 18; Indels 0
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="RPCI-23-92L24"
/sex="Female"
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/clone_lib="RPCI-23"
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Class: BAC ends.
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CNS01V5E 1inear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 197P20 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                        Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of treshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                          AL168683 G1:7806740
AL168683.1 G1:7806740
GSS; genome survey sequence.
Tetraodon nigroviridis
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                                                                                            selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Industriangle properties"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lone=lib="NIH_MGC_17"
/note="Organ: muscle; vector: pOTB7; Site_1: EcoRI;
/note="Organ: muscle; vector: pOTB7; Site_1: EcoRI;
/note="Organ: muscle; vector: potage using the pirectionally cloned into EcoRI/XhoI sites using the following s' adaptor: GGCACAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE300265 1018 bp mRNA linear EST 20-JUL-2000 600944030T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960382 3',
                                                                                                                                                                                                                                                                       ö
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
CoORI: Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DRA was isolated and partially digested
with a combination of EcoRI and ECORI Methylase. Size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1018)

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMS3 row: k column: 07
High quality sequence start: 23
High quality sequence
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                                                                                                                                                                                                                        DB 28; Length 538;
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                                                                                                                                                                                                                     Score 28.4; D
Pred. No. 46;
0; Mismatches
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Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2960382"
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                                                                                                                                                                                                                     ch 47.3%;
l Similarity 70.4%;
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
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Best Local Similarity
Matches 38; Conserv
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TITLE
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BE300265
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Direct Submission
Submitted (12-APR-2000) Genoscope – Centre National de Sequencage :
BP 191 91006 EVRY cedex – FRANCE (E-mail : segref@genoscope.cns.fr
                                                       Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                              /clone lib="G"
/note="Genoscope sequence ID : COAG197DH10SP1~end
PUC-Ori"
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 768;
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                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="10anor:
                                                                                                                                                                                                                                                                                                                                                                                                      ch 46.0%; Score 27.6; DB 29; Similarity 46.2%; Pred. No. 87; 24; Conservative 17; Mismatches 11;
                                                                                                                                                                Location/Qualifiers
1. .768
/organism="Tetraodon
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Mus musculus
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BH116316
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Gaps

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16; Indels

0; Mismatches

Conservative

9

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7 GCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGAG

end

us-10-069-056-3.rst

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/eex="Male"

/cell type="Spleen/Brain"

/clone lib="RPCI-24"

/note="Vector: pTARBAC1; Site 1: BamH1; Site 2: BamH1;

/note="Vector: pTARBAC1; Site 1: bamH1; Site 2: BamH1;

/note="Vector: pTARBAC1; produced by Pieter de Jong. The

library was cloned in the pTARBAC1 cloning vector at the

BamH1 sites using Mbol partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BJ438237 Bictyostelium discoideum cDNA linear EST 13-MAR-2C
BJ438237 Dictyostelium discoideum cDNA library, VF Dictyostelium
discoideum cDNA clone ddv36f19 3', mRNA sequence.
Tel: 301 838 0200

Fax: 301 838 0208

Bmail: szhaogutjar.org

Clones are derived from the mouse BAC library RPCI-24. For BAC

Clones are derived from the mouse BAC library availability, please contact Pieter de Jong

library availability, please contact Pieter de Jong

(pdejongmail.cho.org). Clones may be purchased from BACFAC

Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC epge: http://www.cigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Seq primer: SP6

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
1 (bases 1 to 760)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostellum discoideum at the vegetative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 45.7%; Score 27.4; DB 28; Length Best Local Similarity 75.6%; Pred. No. 99; Matches 34; Conservative 0; Mismatches 11; Indels
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Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Email: tshini@genes.nig.ac.jp.
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                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. 562
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="RPCI-24-227B7"
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Dictyostelium discoideum
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BJ438237/c
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Eukarustota; Betheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
B 1 (bases 1 to 562)
S Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,
Russell, D., de Jong, P. and Praser, C.M.
Mouse BAC End Gequences from Library RPCI-24
Unpublished (1999)
Other GSSs: RPCI-24-227B7.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: stratogriggr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
library availability, clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://ww.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 386 row: H column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site_1: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1;
/rote="Vector: pTARBAC1; Site_1: BamH1;
/rote="Vector: pTARBAC1 Site_2: BamH1;
/rote="Vector: ptartially produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
                                                                                        Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Gerran,W., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Tsussell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other GSSs: RPCI-24-386H23.TV
Contact: Shaying Zhao
Department of Enkaryotic Genomics
The Institute for Genomic Research
                    Chordata, Craniata, Vertebrata, Euteleostomi,
Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Pred. No. 88;
0; Mismatches 14; Indels 0;
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="RPCI-24-386H23"
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Mus musculus
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BH068411.1 GI:14888008
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                          Eukaryota, Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 791)
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Best Local Similarity 72.0
Matches 36; Conservative
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EST 13-MAR-2002

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Gaps

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Length 562;

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dev stage="Growth phase"
/clone_lib="Dictyostelium discoideum cDNA library, VF"
                                                                                           Length 760;
                                                                                             45.3%; Score 27.2; DB 12;
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/dev_stage="10-11 day embryo"
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AV142404/c
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                                                                                                                                                                                                                                                                                                                                                               AV222962 RIKEN full-length enriched, 18 days pregnant, placenta and extra embryonic tissue Mus musculus cDNA clone 3830405E08 3' similar to X85183 R.norvegicus mRNA for ras-related GTPase, ragA,
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Transcriptional sequencing: A method for DNA sequencing using RNA
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.go.jp,
WL.http://genome-gsc.riken.go.jp,
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                            Gaps
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                                                                                                                4 GTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA
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/dev_stage="18 days pregnant, adult"
/lab_host="DH10B"
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       Pred. No. 1.2e+02;
0; Mismatches 18; Indels
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/clone="3830405E08"
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/strain="C57BL/6J"
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67.98;
                                         38; Conservative
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AV222962/c
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Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Toshino, M., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV142404 EST 02-JUL-1999 AV142404 Mus musculus C57BL/6J 10-11 day embryo Mus musculus CDNA clone 2810423C19, mRNA sequence.
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                          Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGAGAGAGAGACTCTTTTTTTTTTTTVN 3'], cDNA was
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 282)
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prepared and sequenced in Mouse Genome Encyclopedia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 182;
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Tel: 81-298-36-9145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27; DB 9;
Pred. No. 1.2e+02;
0; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Chie Owa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Rodenta; Sciurognathi, Muridae; Murinae; Mus.

1 (bases 1 to 305)

8 Carnindi,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
Akahira,S., Akiyama,J., Pikuda,S., Pukunishi,Y., Funayama,T.,
Rawi,J., Kkuchi,N., Kojima,Y., Matawa,T., Itoh,M., Izawa,M.,
Rawi,J., Kkuchi,N., Kojima,Y., Matewyama,T., Niitsuma,H., Oda,H.,
Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y.,
Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T.,
RIKEN Mouse ESTE
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 AAGGAGGAATTAAAAATACATTTTAATATCTTGCTGATAAAATAGTAACAT 222
                                                                                                                                                                                          257 AAGGAGGAATTAAAAATACATTTTAATATCTTGCTGATAAAATAGTAACAT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AAGTIGCTATIAAAACTACACTIAAAGAGCIGGIGCATAAAAGAGIAACCT 52
                                                                                                                                                  2 AAGTIGCIATTAAAACTAÇACTTAAAGAGCTGGTGCATAAAAGAGTAACCT 52
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0
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                                                                  Length 282
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                                                              Score 27; DB 9; 1
Pred. No. 1.3e+02;
0; Mismatches 15;
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'mol type="mRNA"
'strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                     clone 2900059G11, mRNA sequence. AVIS4012
                                                                                                                                                                                                                                                                                                        305 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
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                                                                ch 45.0%;
1 Similarity 70.6%;
36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36; Conservative
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Best Local Similarity
Matches 36; Conserv
                                                                                          Best Local Similarity
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                                                                      Query Match
                                                                                                                                                                                                                                                                RESULT 11
AV154012/c
                                                                                                                                                                                                                                                                                                                            DEFINITION
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Barell; Oxford University Press, 1999)."
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High quality sequence start: 13
High quality sequence stop: 783.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13-Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Entamoeba histolytica
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AZ687690/c
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/clone_lib="Entamoeba histolytica Stears Constructed at The
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Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Ventrer, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome .
Sequencing: A Practical Approach, eds. M. Vaudin and B.
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                       /tissue_type="whole body"
/dev stage="13 days embryo"
/clone lib="RIKEN full-length enriched, 13 days embryo
whole body.
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Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
mouse tissues.
visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, 17e1: 301 838 0208
Fax: 301 838 3543
                                                                                                         /organism="Mus musculus"
/mol type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Entamoebidae; Entamoeba.
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High quality sequence stop: 855.
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Class: shotgun
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Matches 36; Conservative
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further details.
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/dionalibe Entamobed histolytica Sheared DNA"
/dionalibe Entamobed histolytica Sheared DNA"
/note="Vector: pH081; Site 1: Bat 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoba histolytica: a
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the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)." Entranceba histolytica
Entranceba histolytica
Entanceba lico 865)
Eloftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 9208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared AZ687690 865 bp DNA linear GSS 14-DEC-2000 ENTJL91TR Entamoeba histolytica Sheared DNA Entamoeba histolytica ö Gaps Gaps 261 TATTAACTCTACAAAAAAAAGAAGTAGAACATAAAAAAGGAAAGTTACAAGA 311 . 0 29 9 TATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA 59 9 TATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA Length 858; Match 45.0%; Score 27; DB 28; Length 865; Local Similarity 70.6%; Pred. No. 1.4e+02; les 36; Conservative 0; Mismatches 15; Indels Query Match
45.0%; Score 27; DB 28; Length 85
Best Local Similarity 70.6%; Pred. No. 1.4e+02;
Matches 36; Conservative 0; Mismatches 15; Indels /organism="Entamoeba histolytica" /mol\_type="genomic DNA" /strain="HM1:IMSS" genomic, genomic survey sequence. AZ687690.1 GI:11824836 GSS.

us-10-069-056-3.rst

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Direct Submission
Submitted (12-ARR-2000) Genoscope - Centre National de Sequencage :
BP 1910 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
         CNS032B1 B91 bp DNA linear GSS 01-SEP-2000 Terraodon nigroviridis genome survey sequence PUC-Ori end of clone 206J09 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                  GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha, Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodont.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosst Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Alaracterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                               Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Bstimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .891
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PUC-Ori"
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DEFINITION
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JOURNAL
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22 7 GCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCAC 유 8

Query Match

44.3%; Score 26.6; DB 29; Length 891;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 14; Indels 0

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3, 2004, 00:54:00

Search completed: June Job time: 1505.5 secs

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HYPOTHETICAL:
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-347-655-1
US-08-647-655-2
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US-09-543-681A-2411
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US-09-543-681A-3704
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US-09-439-313-440
US-09-536-616A-440
US-09-685-166A-440
US-09-685-166A-441
US-08-692-787-47
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US-08-777-010-1
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US-09-480-884A-54
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Maximum Match 100%
Listing first 45 summaries
                                              nucleic search, using sw model
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Pred. No. 0.28;
0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08336345
Patent No. 5814510
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gramichael, Leland E.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF ESQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: PLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,345
FILING DATE:
                                                 US-09-221-107-54
US-09-833-381-496
US-09-543-6818-496
US-09-306-446C-1
US-09-543-6818-2681
US-08-545-528D-1
US-09-107-532R-1083
US-09-107-532R-1083
US-09-1192R-142
US-09-328-352-3053
US-09-328-352-3053
US-09-328-352-2606
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US-09-023-655-955
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NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30753
REFERENCE/DOCKET NUMBER: 7937-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-864/9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5049 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
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Best Local Similarity 67.8
Matches 40; Conservative
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ORGANISM: Par
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RESULT 4
US-08-647-655-2
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1116 GAAGTGTCAATCAAATGTACTTTGCGGGACTTGGTTAGTAAAAGAGTAACATCACCTGA 1174
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Parrieh, Colin R.
APPLICANT: Gruenberg, Allen
APPLICANT: Gruenberg, Allen
APPLICANT: Carmichael, Leland E.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIF: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTEN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,345
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30753
REFERENCE/DOCKET NUMBER: 7937-006
TELECHONE: (212) 790-9090
TELEPAX: (212) 869-8864/9711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5049 base pairs
TYPE: nucleic acid
STRANDENNES: both
                                                                                                                                                                                                                          Sequence 2, Application US/08336345
Patent No. 5814510
GENERAL INFORMATION:
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Best Local Similarity 67.8
Matches 40; Conservative
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STATE: New York
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COMPUTER READABLE FORM:
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GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
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40.7%; Score 24.4; DB 4; Length 565;
Best Local Similarity 66.7%; Pred. No. 5.5;
Matches 34; Conservative 0; Mismatches 17; Indels
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                               CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/00846
FILING DATE: 02-MAY-1994
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
US/08/737,109
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IMMEDIATE SOURCE:
LIBRARY: lambda FixII type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-961-527-15
; Sequence 15, Application US/08961527
; Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: P834(
TELECOMUNICATION) INFORMATION:
TELEPHONE: (301) 309-8514
TELEFRA: (301) 309-8512
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                   LENGTH: 565 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 424
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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US-08-737-109-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20850
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Patent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
LEMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1116 GAAGTGTCAATCAAATGTACTTTGCGGGACTTGGTTAGTAAAAGAGTAACATCACCTGA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SLABAS, Antoni Ryszard
APPLICANT: ELBOROUGH, Kieran Michael
APPLICANT: ERIGHT, Simon William Jonathan
APPLICANT: FRITEM, Philip Anthony
TITLE OP INVENTION: Plant Gene Specifying Acetyl Coenzyme A
TITLE OF INVENTION: Carboxylase and Transformed Plants Containing Same
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405 AGTTGTCGATAAAACAACCAATAAAGAGCTTGCTCATTACAAATTAACGGAACAAG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AGTIGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAG 58
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28.6; DB 2; Length 5049;
Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
42.7%; Score 25.6; DB 4; Length 597;
Best Local Similarity 66.1%; Pred. No. 2;
Matches 37; Conservative 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pillsbury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
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Patent No. 6455688
GENERAL INFORMATION:
                           TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: unknown MOLECULE TYPE: NON (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 67.8%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Proteus mirabilis
5049 base pairs
                                                                                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-09-543-681A-2411
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TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococc Patent No. 6503729
TITLE OF INVENTION: jannaschii
FITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ 1D NOS: 3
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t
                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (28222)...(28222)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (28257)...(28258)
OTHER INFORMATION: n equals a, t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (98343)...(98343)
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc_feature
LOCATION: (103598)...(10398)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (148948)...(148948)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (163385)...(163385)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (191989)...(191989)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
LOCATION: (191995)...(191995)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
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LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (84773)...(84773)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
LOCATION: (84808)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                               LENGTH: 1664976
                                                                                                                                                                                                                                                                          SEO ID NO 1
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                US-09-543-681A-3781

Sequence 3781, Application US/09543681A

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

NUMBER: OF SEQ ID NOS: 8344

SEQ ID NO 3781

LENGTH: 213
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APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTBUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 2709-1002-001

CURRENT FILING DATE: 2000-04-05

PRIOR PRILICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                7045 AAGAAACTATTAAAGCTGCACTTGTGGAGTTTTTTAATGGAAAAGTCACTTTAACTGA 7102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGTTGCTATTAAATTTAATGTAATTAAGATTATCAATCTAAGAATAAAAAAAGGGAGA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAAGTIGCTATTAAAACTACACTTAAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA 59
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                                                                                                              2 AAGTIGCIATIAAAACTACACTIAAAAGAGCIGGIGCAIAAAAGAGIAACCICACCAGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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               DB 4; Length 10993;
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                                                               21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23.8; DB 4;
Pred. No. 7.2;
0; Mismatches 22;
          10 11; Score 24.4; Dilarity 63.8%; Pred. No. 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
1S-09-543-681A-3704/c
'Sequence 3704, Application US/09543681A
; Patent No. 6605709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.7%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA; Proteus mirabilis US-09-543-681A-3704
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Best Local Similarity 62.77
Matches 37; Conservative
Query Match
Best Local Similarity
Matches 37; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3704
LENGTH: 336
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US-08-916-421B-1
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405931 AGTTGAATTTAAAGGAACAATTAGAGAGCTGTTAGATAAAGGA 405973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AGTIGCTATIAAAACTACACTIAAAGAGCTGGTGCATAAAAGA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Samaha, Raymond
APPLICANT: Samaha, Raymond
APPLICANT: Samaha, Raymond
APPLICANT: Zhang, James
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, Lynne
CURRENT FILING DATE: 1000-03-22
EARLIER APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 1999-03-23
MUMBER OF SEQ ID NOS: 121
SEQ ID NO 119
LENGTH: 5428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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39.7%; Score 23.8; E
Best Local Similarity 72.1%; Pred. No. 59;
Matches 31; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                    | NAME/KEY: misc feature | NAME/KEY: misc feature | LOCATION: (1602912)...(1602912) | OTHER INFORMATION: n equals a, t, c, or g | NAME/KEY: misc feature | LOCATION: (1603734)...(1603734) | OTHER INFORMATION: n equals a, t, c, or g | NAME/KEY: misc feature | LOCATION: (1637998)...(1637998) | OTHER INFORMATION: n equals a, t, c, or g | LOCATION: (164854)...(164855) | OTHER INFORMATION: n equals a, t, c, or g | US-08-916-4218-1
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Patent No. 6664446
GENERAL INFORMATION:
                  NAME/KEY: misc feature
LOCATION: (1349473)...(1349473)
OTHER INPORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1349491)...(1349491)
OTHER INPORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (147091)...(147091)
NAME/KEY: misc feature
LOCATION: (1569020)
OTHER INPORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1569020)
OTHER INPORMATION: n equals a, t,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Heard, Jacqueline
APPLICANT: Broun, Pierre
APPLICANT: Ricchmann, Jose-Luis
APPLICANT: Keddis, James
APPLICANT: Pineda, Omaira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Arabidopsis thaliana
OTHER INFORMATION: n equals a,
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COTHER INFORMATION: G374
US-09-533-029-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-533-029-119
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3 AGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAAACTCTCA 54
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CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT PILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FeatSEQ for Windows Version 3.0
LENGTH: 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 depler, William
ENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
ENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23.2; DB 4; Length 523; Pred. No. 15; O; Mismatches 18; Indels
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CURRENT APPLICATION NUMBER: US/09/685,166A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ).09-685-166A-440/c
Sequence 440, Application US/09685166A
Patent No. 6630305
                                                                                                                           Sequence 440, Application US/09636215
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      iang, Yuqui
lenderson, Robert A.
alos, Michael D.
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Kalos, Michael D.
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Harlocker, Susan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 65.4%;
Matches 34; Conservative
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Skeiky, Yasir A.W.
Hepler, William
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Vedvick, Thomas S
Carter, Darrick
                                                                                                                                                                                                      Xu, Jiangchun
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Day, Craig H.
Vedvick, Thomas
Carter, Darrick
Li, Samuel
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Retter, Marc W.
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CORGANISM: Homo sapiens
US-09-636-215-440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAAACCTCA 54
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APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Jiang, Yuqui
APPLICANT: Mitcham, Janngchun
APPLICANT: Mitcham, Janngchun
APPLICANT: Mitcham, Jannifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REPERENCE: 2.10.10.6 PROSTATE CANCER AND METHODS FOR THEIR USE
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT APPLICATION NUMBER: US/09/352,616A
NUMBER OF SEQ ID NOS: 472
SOUTHWARE: FeatSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                  1328 GAAATATCTATTGATCCGCCACTGAGAGAACTGGTGCAAAACAAATGA 1376
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                                    1 GAAGTTGCTATTAAAACTACACTTAAAAGAGCTGGTGCATAAAAGAGTAA 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Raige, Michael APPLICANT: Fanger, Gary APPLICANT: Fanger, Gary APPLICANT: Retter, Mark APPLICANT: Retter, Mark APPLICANT: Solk, John Title OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.42709
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23.2; DB 4; Length 5; Pred. No. 15; 0; Mismatches 18; Indels
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4.09-352-616A-440/c.
; Sequence 440, Application US/09352616A
; Patent No. 6395278
                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Jiangchun C. APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan Louise APPLICANT: Harlocker, Sugul APPLICANT: Reed, Steven G. APPLICANT: Reed, Steven G. APPLICANT: Kalos, Michael
                                                                                                                                                                                                        Sequence 440, Application US/09439313
Patent No. 6329505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 38.7%;
Best Local Similarity 65.4%;
Matches 34; Conservative (
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CORGANISM: Homo sapiens
US-09-352-616A-440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA; ORGANISM: Homo sapiens
US-09-439-313-440
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Best Local Similarity
Matches 34; Conserv
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US-09-439-313-440/c
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LENGTH: 523
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LENGTH: 523
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Gaps

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; CURRENT FILING DATE: 2000-10-10; NUMBER OF SEQ ID NOS: 898; SOFTWIRE: FastSEQ for Windows Version 3.0; SEQ ID NO 440; SEQ ID NO 440; SEQ ID NO 440; TYRE: DAA; TYRE: DAA; TYRE: DAA; TYRE: DAA; ORGANISM: HOmo sapiens US-09-685-166A-440

Query Match
Best Local Similarity 65-4%; Pred. No. 15; Best Local Similarity 65-4%; Pred. No. 15; Matches 34; Conservative 0; Mismatchés 18; Indels 0; Gaps 0;
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Search completed: June 3, 2004, 00:56:17 Job time: 36.75 secs

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2, 2004, 23:14:04; Search time 141 Seconds (without alignments) 1941.275 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/DEAT PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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60
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                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
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18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBGOMB.seq:\*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Sequence 15566,	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 230058	Sequence 230058	Sequence 2616, Ap	Sequence 154079,	Sequence 154080,	Sequence 154079	Sequence
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		US-10-282-122A-15566	US-10-027-632-56680	US-10-027-632-75051	US-10-027-632-56680	US-10-027-632-75051	-3694	-3694	US-10-027-632-230058	US-10-027-632-230058	2616	US-10-027-632-154079	US-10-027-632-154080	US-10-027-632-154079	US-10-027-632-154080
IES		2-122	7-632	7-632	7-632	7-632	US-10-027-632-3694	US-10-027-632-3694	7-632	7-632	JS-09-880-107-2616	7-632	7-632	7-632	7-632
SUMMARIES		10-28	10-02	10-02	10-02	10-02	10-02	10-02	10-02	10-02	9-880	10-02	10-02	10-02	10-02
เร	ID	Su	ns-:	ns-:	ns-:	ns-	SU	US-	ns-	US-:	US-0	us-	ns-:	ns-	ns-
	DB	13	13	13	16	16	13	16	13	16	6	13	13	16	16
	Query Match Length DB	2931	502	502	502	502	672	672	597	597	388	925	925	925	925
df	Query	43.7	43.0	43.0	43.0	43.0	43.0	43.0	42.7	42.7	42.3	41.7	41.7	41.7	41.7
	Score	26.2	25.8	25.8	25.8	25.8	25.8	25.8	25.6	25.6	25.4	25	25	25	25
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	24.6	41.0	2000	1	US-09-938-842A-2977	Sequence 2977,
	24.6	41.0	2940	13	US-10-027-632-111618	Seguence 111618,
	24.6	41.0	2940	16	US-10-027-632-111618	Sequence 111618
	24.4	40.7	419	6	US-09-983-965-61	Sequence 61, Appl
	24.4	40.7	10993	13	US-10-158-844-15	Sequence 15, A
	24.4	40.7	00996	12	US-09-997-722-85	Sequence 85, A
	24.2	40.3	1260	13	US-10-425-114-10451	Sequence 10451
	24.2	40.3	1262	13	US-10-424-599-54636	Sequence 54636
	24.2	40.3	8951	15	US-10-311-455-768	
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	24	40.0	446	2	US-09-918-995-23611	
	24	40.0	451	13	US-10-027-632-40376	
	24	40.0	451	16	US-10-027-632-40376	Sequence 40376
	24	40.0	1012	13	US-10-027-632-100959	Sequence 10095
	24	40.0	1012	13	US-10-027-632-100960	
	24	40.0	1012	16	US-10-027-632-100959	Sequence 100959,
	24	40.0	1012	16	US-10-027-632-100960	
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	24	40.0	107829.	13	US-10-087-192-361	Sequence 361, App
	23.8	39.7	193	13	US-10-424-599-84615	
	23.8	39.7	33991	12	US-09-997-722-109	Sequence 109, App
	23.6	39.3	322	13	US-10-027-632-14611	1461
	23:6	39.3	322	16	US-10-027-632-14611	
	23.6	39.3	582	13	US-10-027-632-221768	Sequence 221768,
	23.6	39.3	582	16	US-10-027-632-221768	Sequence 221768
	23.6	39.3	603	13	US-10-027-632-130629	Sequence 130629
	23.6	39.3	603	16	US-10-027-632-130629	Sequence 13062

#### ALIGNMENTS

US-10-282-122A-1556

US-10-282-122A-1556

Sequence 1556, Application US/10282122A

Publication No. US20040029129A1

GENERAL IMPORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Wallow, Carlos

APPLICANT: Wallow, Carlos

APPLICANT: ApplicANT: Obleen, Kari

APPLICANT: Travick, John

APPLICANT: Wall, Daniel

APPLICANT: Wang, Liangel

APPLICANT: Travick, John

APPLICANT: Yamanch, Robert

PRIOR APPLICATION NUMBER: 60/230, 347

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-01-27

PRIOR PILING DATE: 2000-01-27

PRIOR PILING DATE: 2000-10-27

PRIOR PILING DATE: 2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 44;
0; Mismatches
                                              PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTERQ for Windows Version 4.0
SERICTH: 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 56680, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
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73.3%;
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Best Local Similarity 73.3
Matches 33; Conservative
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ORGANISM: Human
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Object of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/02/04.30
PRIOR PILING DATE: 2002-04-20
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-10-23
PRIOR PILING DATE: 1999-10-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-10-28
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                          Length 2931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1091 AAGAAGTAGTTAAAATACACTTAAAGAGCTTGTTAAAAATGGAATA 1137
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Pred. No. 44;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AAGTIGCTAITAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTA
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Pred. No. 55;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20020198371A1
                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-15566
                                                                                                                                                                                                                                                                                                                                                                        Query Match 43.7%;
Best Local Similarity 72.3%;
Matches 34; Conservative
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Best Local Similarity 73.3
Matches, 33; Conservative
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US-10-027-632-75051/c
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US-10-027-632-56680/c
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US-10-027-632-56680
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LENGTH: 502
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LENGTH: 2931
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Gaps

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DB 13; Length 502;

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GENERAL ILVERMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR PLICATION NUMBER: US 60/198,676

PRIOR PLING DATE: 2000-07-12

PRIOR PLING DATE: 2000-04-20

PRIOR PLING DATE: 2000-04-20

PRIOR PLING DATE: 2000-03-24

PRIOR PLING DATE: 2000-03-24

PRIOR PLING DATE: 2000-02-24

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-109-28

PRIOR PLING DATE: 1999-109-28

PRIOR PLING DATE: 1999-09-28

PRIOR PLING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SEQ ID NO 56680

LENGTHA SOFTWARE: FBSEEQ for Windows Version 4.0

SEQ ID NO 56680
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Pred. No. 44;
0; Mismatches
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Best Local Similarity 73.3 Matches 33; Conservative
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Gaps

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US-LIVUAZI-62-26-36-36

Sequence 3694, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPRESENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR PELICATION NUMBER: US 60/128,006

PRIOR PELICATION NUMBER: US 60/199,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/195,218

PRIOR PELING DATE: 2000-03-24

PRIOR PELING DATE: 2000-03-24

PRIOR PELING DATE: 1999-11-23

PRIOR PELING DATE: 1999-10-23

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-80-9

PRIOR FILING DATE: 1999-09-80-9

PRIOR FILING DATE: 1999-09-80-9

PRIOR FILING DATE: 1999-09-80-9

SOFTWARE: FastESQ for Windows Version 4.0

SEQ ID NO 3694

LENGTH: 672

LENGTH: 672
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERRINCE: 108927.129
CURRENT APPLICATION NUMBER: US/10/027,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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43.0%; Score 25.8; DB 16; Length 672;
Best Local Similarity 73.3%; Pred. No. 48;
Matches 33; Conservative 0; Mismatches 12; Indels 0
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Pred. No. 48; OB Mismatches
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; Sequence 230058, Application US/10027632
; Publication No. US20020198371A1
; TYPE: DNA; Human; OKGANISM: Human; PEATURE:
; NAME/KEY: misc_feature; LOCATION: (1)...(672); OTHER INFORMATION: n = A,T,C or GUS-10-027-632-3694
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Best Local Similarity 73.3%;
Matches 33; Conservative
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                                                                                                       Sequence 75051, Application US/10027632
Publication No. US2003020407549
FUBLICANITY MANGY DAVID GENERAL INFORMATION:
APPLICANITY WANGY DAVID GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR APPLICATION NUMBER: US 60/218,006
FRIOR PRIOR APPLICATION NUMBER: US 60/198,676
FRIOR PRIOR APPLICATION NUMBER: US 60/193,483
FRIOR FILING DATE: 2000-04-20
FRIOR PELING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-00-224
FRIOR PELICATION NUMBER: US 60/156,358
FRIOR FILING DATE: 1999-00-224
FRIOR FILING DATE: 1999-00-28
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108927.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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0; Mismatches 12;
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Pred. No. 44
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PRIOR PELING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PELING DATE: 1000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 75051
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 73.3
Matches 33; Conservative
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US-10-027-632-75051
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Gaps

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1 GAAGTIGCIATIAAAACTACACTIAAAGAGCIGGIGCATAAAAGAGTAACCICACCAGA 59
                                                                             Sequence 2616, Application US/09880107

Factor No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: HORNE, Darci T.

APPLICANT: Scherf, Uwe

APPLICANT: Scherf, Uwe

TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT PILING DATE: 2001-06-14

PRIOR PILING DATE: 2000-06-14

PRIOR PILING DATE: 2000-06-14

PRIOR PILING DATE: 2000-06-14

PRIOR PILING DATE: 2000-06-14

PRIOR PILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2616

LENGTH: 388
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US-09-880-107-2616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
42.3%; Score 25.4; DB 9; Length 388;
Best Local Similarity 64.4%; Pred. No. 55;
Matches 38; Conservative 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
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US-10-027-632-154079
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Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR PAPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-08-09

PRIOR FILING DATE: 1999-09-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR APPLICATION NUMBER: US 60/146,002
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-3
PRIOR FILING DATE: 1999-09-3
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FRANCE FOR WINDOWS VERSION 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 63.84
Best Local 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.8
Matches 37; Conservative
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US-10-027-632-230058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-027-632-230058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 230058
LENGTH: 597
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LENGTH: 597
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                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVERTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT PILING DATE: 2002-04-30

PRIOR PLICATION NUMBER: US 60/118,006

PRIOR PLICATION NUMBER: US 60/118,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR PLICATION NUMBER: US 60/193,483

PRIOR PLICATION NUMBER: US 60/193,483

PRIOR PLICATION NUMBER: US 60/185,218

PRIOR PLICATION NUMBER: US 60/165,363

PRIOR PLICATION NUMBER: US 60/167,363

PRIOR PLICATION NUMBER: US 60/167,363

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-10-24

PRIOR PLING DATE: 1999-09-28

PRIOR PLING DATE: 1999-09-28

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-08-09

PRIOR PLING DATE: 1999-08-08

PRIOR PLING DATE: 1999-08-09

PRIOR PLING DATE: 1999-08-09
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Pred. No. 1e+02;
0; Mismatches 15; Indels
US-10-027-632-154079
; Sequence 154079, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
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Best Local Similarity 69.4%;
Matches 34; Conservative
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493 GAAATTAATAAGCCATCCATAGTTAAAGAGCTAGTGAATGACAGAGTAA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAA 49
                                                                                                                                                                                                                                                                                                                         DB 16; Length 925;
le+02;
ches 15; Indels
                                                                                                                                                                                                                                                                                                                              Score 25; DB 3
Pred. No. 1e+03
0; Mismatches
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 154079
LENGTH: 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 56717, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              41.7%;
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Best Local Similarity 69.4%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 69.43
Matches 34; Conservative
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US-10-027-632-154080
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US-10-027-632-154080
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                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REPERBUCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-33
PRIOR PILING DATE: 1999-11-33
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-8
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                                                                                                493 GAAATTAATAAGCCATCCATAGTTAAAGAGCTAGTGAATGACAGAGTAA 541
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                                                  GAAGTIGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 41.7%; Score 25; DB 13; Length 925; Best Local Similarity 69.4%; Pred. No. 1e+02; Matches 34; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAA
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                                                                                                                                                                                                                                                                                                                         Sequence 154080, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                  RESULT 12
US-10-027-632-154080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Human
US-10-027-632-154080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-027-632-154079
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: ANO VIDE David K
APPLICANT: Chou Vibua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           493 GAATTAATAAGCCATCCATAGTTAAAGAGCTAGTGAATGACAGAAAA 541
                                                                                                                                                                                                                                                                                                                                                                                                  Length 925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAA
                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 16;
Pred. No. 1e+02;
0; Mismatches 15
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0;
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                                                                                                                                                                                                                                                                                9 TATTAAAACTACACTTAAAGAGTGCATAAAAGAGTAACCTCACCAGAG 60
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 56717
ILENGTH: 1844
; TYPE: DNA
ORGANISM: Glycine max
; FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_22226C.1
US-10-424-599-56717
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Search completed: June 3, 2004, 03:14:05 Job time: 142 secs

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(without alignments)
118.967 Million cell updates/sec
                                                                                                                                                    May 28, 2004, 12:48:18 ; Search time 47.5 Seconds
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                      OM protein - protein search, using sw model
                            Copyright
                                                                                                                                                    Run on:
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1 EVAIKTTLKELVHKRVTSPE 20 BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-069-056-5 97 Scoring table: score: Sequence: Perfect

1586107 Total number of hits satisfying chosen parameters:

1586107 seqs, 282547505 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% .Maximum Match 100%

geneseqD1980s: \*
geneseqD2000s: \*
geneseqD2000s: \*
geneseqD2001s: \*
geneseqD2001s: \*
geneseqD2003s: \*
geneseqD2003bs: \*
geneseqD2003bs: \* A\_Geneseq\_29Jan04:\* 1: qeneseqp1980s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

uo	Parvoviru	Parvoviru	Parvoviru	Parvoviru	Parvoviru	Parvoviru	Sequence	Novel hum	Talin C-t	Enterohae	Human pre		Hexos	Human ORF	Human Tal	Breast ca	Rat Prote	Human Pro	Rat Prote	Human Pro	Protein 's	Human pro	Human pol	Human pol	Human str
Description	Aay72703	Aay72704	Aay72708	Aay72710	Aay72706	Aay72702	Aap40306	Abg03712	Aar76871	Adc01077	Abg70144	Abg70135	. Aaw85601	Aab41087	Abb81459	Abr47614	Ade58866	Add45522	Add45520	Ade58868	Abr53759	Aam79794	Aam41079	Aam41098	Aae33668
ΩI	AAY72703	AAY72704	AAY72708	AAY72710 ·	AAY72706	AAY72702	AAP40306	ABG03712	AAR76871	ADC01077	ABG70144	ABG70135	AAW85601	AAB41087	ABB81459	ABR47614	ADE58866	ADD45522	ADD45520	ADE58868	ABR53759	AAM79794	AAM41079	AAM41098	AAE33668
88	4	4	4	4	4	4	Н	4	~	7	Ŋ	Ŋ	~	ო	'n	9	7	7	7	7	9	4	4	4	9
Length DB	20	672	672	672	672	672	069	674	200	250	548	698	777	2541	2541	2541	2541	2541	2541	2541	166	1177	1177	1177	2542
% Query Match	100.0	100.0	6.96	96.9	6.96	96.9	59.8	47.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	45.4	45.4	45.4	45.4	45.4
Score	97	97	94	94	94	94	28	46	45	45	45	45	45	45	45	45	45	45	. 45	45	44	44	44	44	44
Result No.	-1	7	ო	4	Ŋ	v	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

	Yeast Sen	Saccharom	Arabidops	Arabidops	Arabidops	Protein a	Protein e	Human MDD	Novel hum	Lung-spec	Human sec	Human pro	Human pol	Human L-i	Alloiococ	Aspergill	Human DIT	Human pol	Human sec
Abu65078	Aay77815	Abw01202	Aag31112	Aag31111	Aag31110	Abr53451	Abu25772	Abu11579	Abg11447	Aao21805	Aag00595	Aab93292	Abp62932	Abg31585	Adb09803	Aaw31628	Abr41168	Aa012652	Abr40559
ABU65078	AAY77815	ABW01202	AAG31112	AAG31111	AAG31110	ABR53451	ABU25772	ABU11579	ABG11447	AA021805	AAG00595	AAB93292	ABP62932	ABG31585	ADB09803	AAW31628	ABR41168	PA012652	ABR40559
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2545	471	472	1034	1069	1121	2000	66	431	1005	99	91	361	361	361	378	397	413	112	160
45.4	44.8	44.8	44.8	44.8	44.8	44.8	44.3	44.3	44.3	43.3	43.3	43.3	43.3	43.3	43.3	43.3	43.3	42.8	42.3
44	43.5	43.5	43.5	43.5	43.5	43.5	43	43	43	42	42	42	42	42	42	42	42	41.5	41
26	2.1	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant. Parvovirus non-structure protein 1 (NS1) variant (S283A) peptide. Location/Qualifiers AAY72703 standard; peptide; 20 AA. (revised)
(first entry) Key Misc-difference 06-AUG-2003 31-MAY-2001 Parvovirus. Synthetic AAY72703; RESULT 1 

/note= "Wild type Ser substituted with Ala; This location corresponds to position 283 of the NS1 variant (S283A) shown in AAY72704" 99EP-00115161. 99EP-00115161 EP1077260-A1. 13-AUG-1999; 13-AUG-1999; 21-FEB-2001.

Rommelaere J; WPI; 2001-212717/22. N-PSDB; AAD02798. Nueesch J,

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.

Disclosure; Page 14; 41pp; English.

The present sequence is a peptide fragment of parvovirus non-structure protein 1 (NS1) variant (S283A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
cytotoxicity activity. These variants are useful as toxins for treating
                                                                                                                                                                                                                                                                                                                                                                                              NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
              tumoural diseases. The variant DNAs are useful as vectors for gene .therapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild type Ser substituted with Ala"
                                                                                       100.0%; Score 97; DB 4; Length 20; 100.0%; Pred. No. 2.4e-09;
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                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                Parvovirus non-structure protein 1 (NS1) variant (S283A)
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                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 14-16; 41pp; English.
                                                                                                                                                                                                                                                            AAY72704 standard; protein; 672 AA.
                                                                                                                                                   EVAIKTILKELVHKRVTSPE 20
                                                                                                                                                                               EVAIKTIKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99EP-00115161.
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                                                                                       Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nueesch J, Rommelaere J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                      (revised)
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N-PSDB; AAD02799.
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Best Local Similarity
Matches 20; Conserv
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Misc-difference
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                                                             Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                             Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                              RESULT 2
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The present sequence is parvovirus non-structure protein 1 (NSI) variant (T394A). The invention relates to the variants of the parvovirus non-structure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                   NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
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                                                                                                                                                                                                                                                                                                                        /note= "Wild type Thr substituted with Ala"
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                                                                                                                                                                        Parvovirus non-structure protein 1 (NS1) variant (T394A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 EVSIKTTLKELVHKRVTSPE 300
281 EVAIKTILKELVHKRVTSPE 300
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                                                                       AAY72708 standard; protein; 672
                                                                                                                                                                                                                                                                                                                                                                                                             99EP-00115161.
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(first entry)
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Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nueesch J, Rommelaere J;
                                                                                                                                (revised)
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                                                                                                                                                                                                                                                                                                          Misc-difference 394
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31-MAY-2001
                                                                                                                                06-AUG-2003
                                                                                                                                                                                                                                                  Parvovirus
                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                    AAY72708;
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                                          RESULT 3
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1 EVALKTILKELVHKRVTSPE 20

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The present sequence is parvovirus non-structure protein 1 (NS1) variant (7854A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Length 672;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 94; DB 4; Le.
Pred. No. 4.8e-07;
1; Mismatches 0;
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                                                                                                                                                  (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
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                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 19-21; 41pp; English
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                                                                          99EP-00115161
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Best Local Similarity 95.0%;
Matches 19; Conservative
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(first entry)
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                                                                                                                                                                                       Rommelaere
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N-PSDB; AAD02797.
                                                                                                                                                                                                                                             N-PSDB; AAD02801
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EP1077260-A1
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31-MAY-2001
                                     21-FEB-2001
                                                                                                                                                                                       Nueesch J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is parvovirus non-structure protein 1 (NS1) variant (T463A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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                                 NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 672;
Parvovirus non-structure protein 1 (NS1) variant (T463A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 94; DB 4; I
Pred. No. 4.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                              (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 30-32; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Nueesch J, Rommelaere J;
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Best Local Similarity 95.0
Matches 19; Conservative
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31-MAY-2001
                                                                                           Parvovirus.
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                                                                                                               Synthetic
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AAY72706 RESULT

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The present sequence is a parvovirus wild-type non-structure protein 1 (NS1). The present invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The inventors claim an immunologically active polypeptide for the development of vaccinal immunity against parvovirus infection. Also claimed are DNA sequences wholly or partly duplicative of defined sequences. The polypeptides are used in vaccines for conferring protection against parvovirus infections in man and animals. (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence encoded by the double-stranded replicative form DNA of porcine
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transcription activities, and cytotoxic activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porcine parvovirus; NADL-2 virulent strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP40306 standard; protein; 690 AA
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                                                                         Disclosure, Fig 1, 41pp, English
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84US-00567968
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12-JAN-1992
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The Invention Fetales to isolated polymetracide (11) and pulpeptide (11) reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymolocides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of stees expressing (II). (II) and (II) are useful for treating disorders in polypeptide and polymolectide sequences have applications in dispnostics, forensics, gene mapping, identification of mutations in diagnostics, forensics gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at Esquences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.4%; Score 46; DB 4; Length 674; 56.2%; Pred. No. 68; 3; Indels iive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID NO 34071; 103pp; English
                                                                                                                                                                                                                                              Novel human diagnostic protein #3703
                                                                                                                                    Ź
                     282 EVSIKCTIRDLVNKRCTSIE 301
 20
                                                                                                                                ABG03712 standard; protein; 674
1 EVAIKTTLKELVHKRVTSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 KTTLKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS67899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 674 AA;
                                                                                                                                                                                                                                                                                                                                                                                W0200175067-A2
                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity
                                                                                                                                                                                                           13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2001
                                                                                                                                                                       ABG03712;
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Gaps

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Score 58; DB 1; Length 690; Pred. No. 0.64; 5; Mismatches 3; Indels

Query Match
Best Local Similarity 60.0%;
Matches 12; Conservative

(first entry)

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The invention relates to a novel enterohaemorragic Escherichia coli 0157:H7-specific nucleic acid molecule. A polynucleotide of the invention has anti-bacterial activity. The polypeptide can be used in detection and/or treatment of 0157:H7 infection. The nucleotide sequence of the genome of Enterohaemorragic E coli 0157:H7 was determined. The present sequence represents an E. coli 0157:H7-specific polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterohemorragic Escherichia coli 0157:H7-specific nucleic acid molecule and a polypeptide and its use, a polypeptide, a vector and a host cell.
                                                                                                                         Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 1121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; SEQ ID NO 1121; 2067pp; Japanese.
                  ADC01077 standard; protein; 250 AA.
                                                                                                                                                            enterohaemorragic; anti-bacterial.
                                                                                                                                                                                                                                                                                                                                            24-JAN-2001; 2001JP-00112010.
                                                                                                                                                                                                                                                                                                        24-JAN-2002; 2002JP-00015959
                                                                                                                                                                                                Sscherichia coli; 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                             (UYTS-) UNIV TSUKUBA
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-451640/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 250 AA;
                                                                                                                                                                                                                                   JP2002355074-A.
                                                                                       04-DEC-2003
                                                                                                                                                                                                                                                                       10-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
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ADC01077
                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Talin binds to vinculin and this is reduced on incubation with, e.g. Vinl Talin binds to vinculin and this is reduced on incubation with, e.g. Vinl 2.1. Vinl2.1 is a specific vinculin binding peptide generated from a TSAR (Totally Synthetic Affinity Reagent) 12 library. Many changes at the Neternatus are not disruptive whereas most changes at the C-terminus are disruptive. Mutagenesis of Vinl2.1 was carried out deliberately contaminating the precursor reservoirs used to construct the contaminating the precursor reservoirs used to make mutated phage. The vinculin binding TSARs may alter the mobility or attachability of malignant cells, perhaps preventing or inhibiting metastasis. The TSARs are new and/or improved heterofunctional binding fusion porteline that have affinity for the ligand vinculin, and can be used to modulate the activity of the paramaceuticals, etc. Other TSARs can be designed to bind dynein and glutathione-S-transferase. Typical applications are: (i) inhibition of GST to treat cancers that produce high levels of this enzyme; (ii) attention mobility/atteachment of malignant cells, modulating placelet release and blood clotting, for TSARs directed against vinculin; (iii) TSARs against dynein are used to modulate nerve cell activity, sperm motility, mobility of protozoa, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying peptide(s) that bind specifically to dynein, vinculin or enzymes, eg. glutathione-S-transferase - by screening random peptide libraries, useful e.g. in immunoassays, affinity purification., tumour treatment, etc.
                                                                                                                                                                                                                                 totally synthetic affinity reagent; vinculin; dynein; enzyme; heterobifunctional binding fusion protein; glutathione S-transferase; cancer treatment; nerve cell activity; modulate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.4%; Score 45; DB 2; Length 200; 55.6%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 7.2.4; Page 65; 110pp; English.
                                                                                         AAR76871 standard; peptide; 200 AA
 382 RTCLKDSVHQRVSSAE 397
                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-US001286
                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-00189331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                            (first entry)
                                                                                                                                                                                                ralin C-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-275411/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adey NB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 200 AA;
                                                                                                                                                            08-MAY-1996
                                                                                                                                                                                                                                                                                                                                            WO9520601-A1
                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                               03-AUG-1995
                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                         AAR76871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kay
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Prey protein; ospB; ospDl; ipaD; ipaH9.8; ospG; ospCl; Shigella; shigellosis; bacillary dysentery; antibacterial; yeast two-hybrid system; protein-protein interaction; SID; selected interacting domain; human.
                                                                                                                                                                       Human prey protein for Shigella ipaC #8.
                                                                                         ABG70144 standard; protein; 548 AA
                                                                                                                                                                                                                                                                                                                                   11-JAN-2002; 2002WO-EP000777
                                                                                                                                                                                                                                                                                                                                                            12-JAN-2001; 2001US-0261130P.
               | ||: :|| :| |
183 TLLKDFIHKHITRP 196
6 TTLKELVHKRVTSP 19
                                                                                                                                              21-OCT-2002 (first entry)
                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                          25-JUL-2002,
                                                                                                                    ABG70144;
                                                                                            CXXXEXEXEXEXEXEXEX
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Gaps ö

5; Indels

3; Mismatches

Best Local Similarity 55.6 Matches 10; Conservative

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Gaps

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Score 45; DB 7; Length 250; Pred. No. 31; 3; Mismatches 4; Indels

46.4%;

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Legrain P;

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The invention relates to a complex of protein-protein interactions

between a Shigella flexneri polypeptide (e.g. ospB, ospD, ipaD, ipaC,

content a Shigella flexneri polypeptide defined in the

specification. The complexes are formed using the yeast two-hybrid

conficient and specification in the sector a modulating compound obtained from the method of (2); (4) a SID

comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a

comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a

containing the vector; and (10) a protein comprising the conding the above polypeptide and a mammalian polypeptide defined in the containing the vector; and (10) a protein comprising the compound, containing the vector; and (10) a protein comprising the compound, containing the vector; and (10) a protein comprising the compound, containing the vector; and (10) a protein comprising the compound, containing the vector; and (10) a protein for treating or preventing chigellosis (bacillary dysentery) in a human or mammal. The present sequence represents a human prey protein isolated by the yeast two-hybrid assay, forming a complex of the invention with a shigella protein
                                                                                                 flexneri polypeptide and a prey mammalian or human placenta polypeptide for treating or preventing bacillary dysentery in a mammal or human.
                                                                              New complex of protein-protein interactions between a bait Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hexosaminidase; enzyme; laundry; cleaning agent; hydrolysis;
anti-microbial; detergent; surfactant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 5; Length 698; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                     Claim 7; Page 98-99; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW85601 standard; protein; 777 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 AIAVTVQEMVTKSNTSPE 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US009125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0045756P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AIKTTLKELVHKRVTSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROC ) PROCTER & GAMBLE CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.6'
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hexosaminidase enzyme.
WPI; 2002-599706/64.
N-PSDB; ABS51528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 698 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9850512-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-1999
02-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW85601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW85601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a complex of protein-protein interactions between a Shigella flexneri polypeptide (e.g. ospB, ospB), ipaD, ipaC, ipaH9.84 ospG and ospCl) and a mammalian polypeptide defined in the specification. The complexes are formed using the yeast two-hybrid system. Also included are (1) a recombinant host cell expressing the interactions between the Shigella flexneri polypeptide and amammalian polypeptide defined in the specification; (2) selecting a mammalian polypeptide defined in the specification; (2) selecting a modulating compound obtained from the method of (2); (4) as 1D computating compound obtained from the method of (2); (5) a SID comprising the human polypeptides appearing as ABG70042-ABG7042; (5) a SID polymelection of its fragment or variant comprising the above polypeptides a vector comprising (3); (6) a recombinant host cell cabove polypeptide avector comprising (3); (6) a recombinant host cell containing the vector; and (10) a protein chip comprising shigella containing the vector; and (10) a protein comprising the compound, polypeptide or polymucleotide is useful for treating or preventing shigelings (bacillary dysentery) in a human or mammal. The present sequence represents a human prev protein moment or mammal. The present sequence represents a human prev protein isolated by the yeast two-hybrid assay, forming a complex of the invention with a shigella protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prey protein, ospB; ospD1; ipaD; ipaC; ipaH9.8; ospG; ospC1; Shigella; shigellosis; bacillary dysentery; antibacterial; yeast two-hybrid system; protein-protein interaction; SID; selected interacting domain; human.
                                                                                                                                                                                New complex of protein-protein interactions between a bait Shigella flexneri polypeptide and a prey mammalian or human placenta polypeptide for treating or preventing bacillary dysentery in a mammal or human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB
Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prey protein for Shigella ipaD #12.
                                                                                                                                                                                                                                                                                       Claim 7; Page 101-102; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG70135 standard; protein; 698 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AIKTTLKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JAN-2002; 2002WO-EP000777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                    WPI; 2002-599706/64.
N-PSDB; ABS51537.
(HYBR-) HYBRIGENICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 548 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200257303-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-OCT-2002
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Gaps

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5; Indels

Laundry and cleaning compositions containing hexosaminidase - to provide

Wolff AM;

Convents AC, Moese RL,

12-JAN-2001; 2001US-0261130P.

ABG70135;

RESULT 12

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(HYBR-) HYBRIGENICS

Legrain P;

WPI; 1999-024116/02.

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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397
            Claim 11; Page 1357; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB81459
                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                         ï
                                                    enzymes (AAW85599-605) can be used in combination in
                                                            an aqueous laundry or cleaning product. The cleaning product is used especially used to launder fabrics and to clean dishes and tableware, particularly in an automatic dishwasher, but may also be used generally as hard surface cleaner. The cleaning product imparts antimicrobial activity and/or eliminates biofilm, the hexosaminidases having a minimum inhibitory concentration of less than about 0.125% but more preferably less than about 0.025%. (NB: entry was revised to change incorrect cross references in Comments field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; noctropic; neuroprotective; anticonvulsant; osteopathic; antiarchritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodespenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; alleryy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                               Length 777;
                                                                                                                                                                                                           h Similarity 40.9%; Pred. No. 1.2e+02; 9; Conservative 8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating e.g. cancers, proliferative disorde
neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ORFX ORF851 polypeptide sequence SEQ ID NO:1702.
antimicrobial activity and remove biofilm.
                                                                                                                                                                                                                                                                                 || ::|:|:|
EVGTVSSLEEIMHGKEKITSPE 673
                                                                                                                                                                                                                                                                                                                                                               AAB41087 standard; protein; 2541 AA
                          Claim 2; Page 39-40; 64pp; English.
                                                                                                                                                                                                                                                                  1 EVAIKTTLKELVH--KRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0127607P.
99US-0127636P.
99US-0127728P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000WO-US008621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-APR-1999; 99US-0127636P.
05-APR-1999; 99US-0127728P.
30-MAR-2000; 2000US-00540763.
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombosis; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leach M;
                                                    Novel hexosaminidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-602362/57.
                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAC75296
                                                                                                                                                                                      Sequence 777 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200058473-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                         AAB41087;
                                                                                                                                                                                                                                                                                              652
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                                                                  AAB41087
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which represent the human OREX open reading frames 1 to 3161. The OREX sequences have activities such as: cytostatic; hepatotropic; vulnerary; cartiporiatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkrinsonian; nootropic; neuroprotective; osteopathic; antiparkrinsonian; neuroprotective; osteopathic; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; cardiant; thrombolytic; antidiamatory; antibacterial; cardiant; thrombolytic; antidiamatory; antidiabetic; hypotensive; cardiant; tantifungal; antitheumatic; antidiamatory; antidiapetic; hypotensive; corpreventing or treating pathological conditions associated with an organization or organization or organization and nucleic acids may be corrected is general disorder. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative cisoreace, organization; hypothyroidism, cholesterol ester disorders, osteoarthritis, graft vs host disease, cardiovascular disease, cidabetes mellitus, hypertension, hypothyroidism, cholesterol ester corrage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes an antisense compound ({\tt I}), 16 to 30 bases in length targeted to specific base regions of a nucleic acid encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, Talin, antimicrobial, antiinflammatory, cytostatic, inhibitor; antisense gene therapy, infection, inflammation, Talin inhibitor; tumour; antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Match 46.4%; Score 45; DB 3; Length 254 Local Similarity 55.6%; Pred. No. 4.8e+02; Local 10; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 13; Col 43-60; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB81459 standard; protein; 2541 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Talin protein SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-OCT-2000; 2000US-00702251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AIKTTLKELVHKRVTSPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISIS-) ISIS PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2541 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABN89190
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human Talin. Also described: (a) an antisense compound up to 30 bases in length which inhibits the expression of human Talin; (b) a composition [II] comprising [I] or (a); and (c) inhibiting the expression of human Talin in human calls or tissues comprising contacting the cells or tissues in vitro with (I) or (a). (I) has antimicrobial, antiinflammatory and expression of activities, and can be used in antisense gene therapy and as a Talin expression inhibitor. (I) can be used: to inhibit the expression of human Talin in human cells or tissues; to prevent or delay infection, inflammation or tumour formation; and in diagnostics, the present sequence represents human Talin from the present invention
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Sequence 2541 AA;

ö 0; Gaps Length 2541; Query Match 46.4%; Score 45; DB 5; Length 254 Best Local Similarity 55.6%; Pred. No. 4.8e+02; Matches 10; Conservative 3; Mismatches 5; Indels

3 AIKTILKELVHKRVTSPE 20

1863 AIAVTVQEMVTKSNTSPE 1880

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Search completed: May 28, 2004, 12:57:02 Job time : 49.5 secs

us-10-069-056-5.rpr

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                 283366 segs, 96191526 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                            1 EVAIKTTLKELVHKRVTSPE 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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97
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Match Length
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1: pir1:*
2: pir2:*
3: pir3:*
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                                                                                                                                          Run on:
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·	30 42 43.3 31 41.5 32 41.42.3 33 41 42.3 34 41 42.3 34 41 42.3 35 41 42.3 36 41 42.3 36 41 42.3 37 41 42.3 38 40.5 41 41.2 40 41.2 41 40 41.2 42 40 41.2 43 40 41.2 43 40 41.2 44 40 41.2 45 40 41.2 45 40 41.2 45 40 41.2 47 40 41.2 48 40 41.2 4	41.5 41.5 41.5 41.5 41.5 41.6 41 41.6 40.6 40.6 40.6 40.6 40.7 40.7 40.7 40.7 40.7 40.7 40.7 40.7	1 42.3 2971 2 TG 5 43.3 2971 2 TG 1 42.3 361 2 TG 1 42.3 1355 2 TG 1 42.3 1355 2 TG 1 42.3 1355 2 TG 1 41.2 238 2 SG 0 41.2 579 2 FG 0 60 60 60 60 60 60 FG 0 60 60 60 60 60 F	43.3 2971 2 T080 42.3 495 2 D694 42.3 481 2 G821 42.3 481 2 G821 42.3 481 2 G821 42.3 1355 2 T070 42.3 1355 2 T7070 42.3 1355 2 T308 41.2 139 2 AC34 41.2 238 2 S752 41.2 238 2 S752 41.2 238 2 S752 41.2 238 2 S752 41.2 579 2 F691	71 2 881 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	10 42 42.3 2971 2 708026  31 41.5 42.8 42.8 495 2 D69310  32 41 42.3 481 2 082125  33 41 42.3 610 2 56568  34 41 42.3 610 2 56568  35 41 42.3 1361 2 T45726  36 41 42.3 1361 2 T45726  37 41 42.3 1361 2 T45726  38 40.5 41.2 1362 2 T45726  39 40.4 12.2 1362 2 T45726  40 41.2 1361 2 T49726  40 41.2 1361 2 T49726  40 41.2 236 2 T49726  40 41.2 236 2 T49726  41 40 41.2 236 2 T49726  42 40 41.2 236 2 S73123  44 40 41.2 236 2 S73123  Approprietion of the sequence revision 17-Feb-1994 #text_change 26-16.5 Febrea 17-Feb-1994 #sequence of parvovirus Iniliand Identification not shown A, McCession: A44276  A, McCession: A44276 MUID: 93297126; PMID: 8517025  A, Fittle: The complete molecules degree of parvovirus Iniliand Identification of shown A, McCession: 1-Feb-1994 #sequence of parvovirus Iniliand Identification of shown A, McCession: 1-Feb-1994 #sequence of parvovirus Iniliand Identification: 1-Feb-1994 #text_change 26-16.5 A, Accession: 1-Feb-1994 #sequence of parvovirus Iniliand Identification: 1-Feb-1994 #text_change 26-16.5 A, Accession: 1-Feb-1994 #sequence 1-Feb-1994 #text_change 16-19.5 Conservative Inilianity 95.0%; Pred. No. 3.6e-07;  Ayinches 19: Conservative I, Mismatches 0; Indels 0; No. 1 EVSIKTTLAELVHKRVTSPE 300  Best Local Smillarity 95.0%; Pred. No. 3.6e-07;  A, Makenies 19: Conservative II; Mismatches 0; Indels 0; No. 1 EVSIKTTLAELVHKRVTSPE 300  RESULT 2  NOW NO. 1 EVSIKTTLAELVHKRVTSPE 300  RESULT 3  NOW NO. 1 EVSIKTTLAELVHKRVTSPE 300  RESULT 6 Febrea 19: Conservative III  NOW NO. 1 EVSIKTTLAELV	hypothetical prote conserved hypothet hypothetical prote hypothetical
	J. Virol A;Title: A;Referer A;Access: A;Molecul A;Cossidu C;Superfe C;KeyworC	Parvov nce num ion: AO io type ss: 1-6 referen amily: 1	73-184, irus ger ber: A03 3695 : DNA 72 <rho> ces: EME parvovir</rho>	1983 tome: n (695; M (187) tome: n (187) tome: n (187) tome: n (187)	TOID TOID TOID TOID TOID TOID TOIL TOIL TOIL TOIL TOIL TOIL TOIL TOIL	J. Virol. 45, 173-184, 1983 J. Virol. 45, 173-184, 1983 A;Title: Parvovirus genome: nucleotide sequence of H-1 and A;Reference number: A03695; MUID:83112183; PMID:6823009 A;Accession: A03695 A;Molecule type: A03695 A;Residus: 1-672 <rho> A;Cross-references: EMBL:X01457; NID:g60993; PIDN:CAA25689. C;Superfamily: parvovirus noncapsid protein C;Keywords: noncapsid protein</rho>	d mapping of its genes by hybric 3.1; PID:g60994; EMBL:J02198
15.7 <u>2.1</u>	Query Match Best Local Matches	Match ocal Sir s 19;	h Similarity 19; Conser	96. larity 95. Conservative	96.9%; 95.0%; ive	Score 94; DB 1; Length Pred. No. 3.7e-07; 1; Mismatches 0; Inde	gth 672; Indels 0; Gaps 0;

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Gaps

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A; Molecule type: DNA

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noncapsid protein NSI - mink enteritis virus (strain Abashiri)
C;Species: mink enteritis virus, MEV
C;Daccies: mink enteritis virus, MEV
C;Daccies: a0-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
C;Accession: A38350
R;Kariatsumari, T.; Horiuchi, M.; Hama, E.; Yaguchi, K.; Ishigurio, N.; Goto, H.; Shinaga J. Gen. Virol. 72, 867-875, 1991
A;Filte: Construction and nucleotide sequence analysis of an infectious DNA clone of the A;Reference number: A38350; MUID:91202123; PMID:2016597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: canine parvovirus, CPV
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: A2962
R;Reed, A.P.; Jones, E.V.; Miller, T.J.
J; Virol. 62, 266-276, 1988
A;Title: Nucleotide sequence and genome organization of canine parvovirus.
A;Reference number: A29962; MUID:88062992; PMID:2824850
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C;Species: feline panleukopenia virus, FPLV
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C;Accession: A36608
A, Residues: 1-392 <CAR>
A, Residues: 1-392 <CAR>
A, Across-references: EMBL:M10824; NID:g333474; PIDN:AAA47160.1; PID:g333475
C, Superfamily: parvovirus noncapsid protein
C; Keywords: noncapsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:M19296; NID:g333438; PIDN:AAA67459.1; PID:g333439 C;Superfamily: parvovirus noncapsid protein C;Keywords: noncapsid protein
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**Residues: 1-668 < KAR>
**Residues: 1-668 < KAR>
**A;Cross-references: GB:D00765; NID:g222435; PIDN:BAA00662.1; PID:g222436
C;Superfamily: parvoirus noncapsid protein
C;Keywords: noncapsid protein
                                                                                                                                                                               Length 392
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Pred. No. 0.00095;
3; Mismatches 2; Indels
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Pred. No. 0.00095;
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                                                                                                                                                                        Score 73; DB;
Pred. No. 0.000
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 EVSIKCTLRDLVSKRVTSPE 301
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EVSIKCTLRDLVSKRVTSPE 301
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Best Local Similarity 75.0%;
Matches 15; Conservative
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Best Local Similarity 75.0
Matches 15; Conservative
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nes 15; Conservative
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A;Molecule type: DNA
A;Residues: 1-668 <REE>
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Best Local Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             noncapsid protein NS1 - minute virus of mice (strain NVMi)

C.Species: minute virus of mice, murine parvovirus
C.Species: minute virus of mice, murine parvovirus
C.Species: minute virus of mice, murine parvovirus
C.Scession: A23008, A25510

R.Sahli, R.; McMaater, G.K.; Hirt, B.
Nucleic Acids Res. 13, 3617-3633, 1985
A.Fitle: DNA sequence comparison between two tissue-specific variants of the autonomous A.Reference number: A23008; MUD:85242059; PMID:385542
A.Recession: A23008
A.Residues: 1-721 < SAH:
A.Residues: 1-72
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('Species: feline panleukopenia virus, FPLV
('Species: deline panleukopenia virus, FPLV
('Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
('Accession: A03697
Ricarlson, J.; Rushlow, K.; Maxwell, I.; Maxwell, F.; Winston, S.; Hahn, W.
J. Virol. 55, 574-587, 1985
A.Title: Cloning and sequence of DNA encoding structural proteins of the autonomous parv
A;Reference number: A03697; MUID:85265017; PMID:2991581
                                                                                                                                                                                                                                                                                                             mice, an autonomous parvovirus.
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                                                                                      A,Molecule type: DNA
A,Residues: 1-645,'I',647-721 <AST>
A;Cross-references: EMBL:M12032; NID:g332289; PIDN:AAA69566.1; PID:g825477
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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95.0%; Pred. No. 4e-07;
live 1; Mismatches
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A;Cross-references: EMBL:V01115
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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1es 19; Conservative
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Matches 19; Conservative
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47.4%;
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Best Local Similarity 60.0*;
Matches 12; Conservative
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Matches 10; Conserv
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A;Molecule type: DNA
A;Residues: 1-85, R', 87-273,'R',275-375,'V',377-620,'NLH',623-624,'PTPPD',630,'AIR',634,
A;Cross-references: ENBL:M38367; NID:g332987; PIDN:AAA46920.1; PID:g332989
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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NyAlternate names: nonstructural protein NS-1
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Accession: 31-Dec-1990 #sequence revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: A36217; A48472; A33743
R;Vasudevacharya, J; Basak, S.; Srinivas, R.V.; Compans, R.W.
A;Trile: The complete nucleotide sequence of an infectious clone of porcine parvovirus, A;Reference number: A36217, MUID:91021005; PMID:2219713
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A; Residues: 1-660 cRAN.
A; Residues: 1-660 cRAN.
A; Cross-references: EMBL:D00623; NID:g303754; PIDN:BAA00501.1; PID:g222358
A; Cross-references: EMBL:D00623; NID:g303754; PIDN:BAA00501.1; PID:g222358
R; Vasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W.
A; Vasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W.
A; Title: The complete nucleotide sequence of an infectious clone of porcine parvovirus, A; Reference number: A36217; MUID:91021005; PMID:2219713
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A, Residues: 1-662 <VAS>
A, Residues: 1-662 <VAS>
A, Residues: 1-662 <VAS>
A, Cross-references: EMBL:M38367, NID:g332987; PIDN:AAA46920.1; PID:g332989
A, Experimental source: strain NADL-2
R, Bergeron, J.; Menezes, J.; Tijssen, P.
Virology 197, 86-98, 1993
A, Title: Genomic organization and mapping of transcription and translation products of
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Cispecies: porcine parvovirus
Cispecies: porcine parvovirus
Cispecies: porcine parvovirus: piaz-Aroca, E.; Casal, J.I.
Cispecies: pirol, 70, 2541-2553, 1989
A; Title: Porcine parvovirus: DNA sequence and genome organization.
A; Reference number: A33302; MUID:90010964; PMID:2794971
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Pred. No. 0.26;
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Pred. No. 0.00095;
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conserved hypothetical protein VC1647 [imported] - Vibrio cholerae (strain N16961 serogro
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: GB:AE004242; GB:AE003852; NID:g9656152; PIDN:AAF94798.1; GSPDB:GN001;
A,Experimental source: serogroup O1; strain N16961; biotype Bl Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RiKaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A; Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein all3180 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 C;Species: Nostoc sp. pCC 7120 C;Species: Nostoc sp. pCC 7120 C;Date: Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AE2203
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A;Cross-references: GB:BA000019; PIDN:BAB74879.1; PID:g17132275; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-662 - SER>
A;Experimental source: strain NADL-2, ATCC VR-742
A;Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBIP:138790)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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22;
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Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                       1; Length 662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
A;Reference number: A48472; MUID:94025614; PMID:8212598
A;Accession: A48472
                                                                                                                                                                                                                                                                                                                                                                                   Score 58; DB 1
Pred. No. 0.26;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.4%; Score 46; DB 62.5%; Pred. No. 22; ive 1; Mismatches
                                                                                                                                                                                                                                                                   C;Superfamily: parvovirus noncapsid protein C;Keywords: noncapsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 EVSIKCTIRDLVNKRCTSIE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVAIKTILKELVHKRVISPE 20
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phosphoenolpyruvate carboxylase (EC 4.1.1.31) isoform C4 (clone ppcA1) - Flaveria trinerv
C,Species: Flaveria trinervia
C,Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                             R;Hermans, J.; Westhoff, P.
Mol. Gen. Genet. 234, 275-284, 1992
A;Title: Homologous genes for the C(4) isoform of phosphoenolpyruvate carboxylase in a C.
A;Reference number: S25081; MUID:92374996; PMID:1508152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AjIntrons: 56/3; 187/2; 215/3; 291/2; 325/3; 355/1; 406/3; 739/3; 868/3
C;Superfamily: phosphoenolpyruvate carboxylase
C;Keywords: carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-967 <HER>
A;Cross-references: EMBL:X64143; NID:g18463; PIDN:CAA45504.1; PID:g18464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 2; Length 967; Pred. No. 35; 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: May 28, 2004, 13:00:57 Job time : 12.5 secs
         135 ESDIEETFKRLVHKLNKSPE 154
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Best Local Similarity 55.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                      C; Accession: S25082
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S18318
Subsphoenolpyruvate carboxylase (EC 4.1.1.31) isoform C4 (clone ppc1-1) - Flaveria trine
C;Species: Flaveria trinervia
C;Date: 22-Nov-1993 #sequence revision 23-Feb-1996 #text_change 22-Jun-1999
C;Accession: S18318; S60517; S17342
R;Poetsex, W.; Hermang, J.; Westhoff, P.
FEBS Lett. 292, 133-136, 1991
A;Title: Multiple cDNA8 of phosphoenolpyruvate carboxylase in the C(4) dicot Flaveria tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule Cype: mRNA
A;Residues: 1-966 <BAUD.
A;Cross-rences: EMBL:225853; NID:g397914; PIDN:CAA81072.1; PID:g397915
C;Superfamily: phosphoenolpyruvate carboxylase
C;Keywords: carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-256, R7, 258-852, S7, 854-966 <POF>
A; Across-references: EMBL:XG1304, NID:9498698; PIDN:CAA43601.1; PID:9498699
A; Cross-references: EMBL:XG1304, NID:9498698; PIDN:CAA3601.1; PID:9498699
A; Note: this is a revision to the sequence from reference S17342
R; Poetsch, W.; Hermans, J.; Westhoff, P.
R; Poetsch, W.; Hermans, J.; Westhoff, P.
A; Description: Multiple CDNAs of the phosphoenolpyruvate carboxylase in the C4 dicot Fla
A; Reference number: S17342
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A;Note: this sequence has been revised in reference $60517
C;Superfamily: phosphoenolpyruvate carboxylase
C;Keywords: carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; phosphoprotein
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                                                                                                                                                                                                       RESULT 13
537072
phosphoenolpyruvate carboxylase (EC 4.1.1.31) - Flaveria australasica
cispecias: Flaveria australasica
cispecias: Flaveria australasica
cipate: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 22-Jun-1999
c;Accession: S37072
R;Bauue, H
R;Bauue, H
R;Reference number: S37072
A;Reference number: S37072
      Gaps
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A;Note: only a part of the coding sequence is given in this paper R;Poetsch, W.
Submitted to the EMBL Data Library, June 1994
A;Reference number: 860517
A;Accession: S60517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 2; Length 966;
Pred. No. 35;
1; Mismatches 8; Indels
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47.4%; Score 46; DB 2; Length 966;
Best Local Similarity 55.0%; Pred. No. 35;
Matches 11; Conservative 1; Mismatches 8; Indels
      5; Indels
Mismatches
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157 EIALSSPSYELIHKRRTS 174
                                                            1 EVAIKTTLKELVHKRVTS 18
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55.0%;
9; Conservative
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Best Local Similarity
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Gaps

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May 28, 2004, 12:48:53; Search time 6.75 Seconds (without alignments) 154.282 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                             Run on:
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US-10-069-056-5 97 1 EVAIKTTLKELVHKRVTSPE 20 Title:
Perfect score: 9
Sequence: 1

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		•			SUMMARIES		
Result		* Query					
No.	Score	Match	Length	DB	ΩI	Description	
-	94	96.9	899	-	VNCS PAVL3	pa	
7	94	9	672	1	VNCS MUMIM	0	
e	94	•	672	-	VNCS MUMIV	P03134 murine minu	
4	94	•	672	Н	VNCS_PAVHH		
2	73	δ.	392	Н	VNCS FPV		
9	73	75.3	668	н	VNCS_FPV19	ĕ	
7	73		899	Н	VNCS_MEVA	mink en	
80	73	75.3	668	Н	VNCS PAVCN	P12929 canine parv	
σ	58	59.8	9	-	VNCS_PAVPN	porcine	
10	28	59.8	662	Н	VNCS PAVPK	porcine	
11	46	47.4	192	Н	Y525 BUCAP	ಹ	
12	46	47.4	996	Н	CAP2_FLATR		
13	46	47.4	996	Н	CAPP FLAAU	Q42730 flaveria au	
14	46	47.4	. 496	-	CAP1 FLATR	Q01648 flaveria tr	
15	45	46.4	777	Н	HEXA_PORGI	porph	
16	45	46.4	2541	Н	TLN1_HUMAN		
17	45	46.4	2541	Н	TLN1 MOUSE		
18	44	45.4	2542	Н	TLN2 HUMAN	Q9y4g6 homo sapien	
19	43.5	44.8	2231	н	SEN1_YEAST		
20	43	٠	186	Н			
21	42	٠	361	Н	CT36_HUMAN		
22	42	43.3	97	н			
23	42	٠	5938	Н	MAC4_HUMAN		
24	41.5	42.8	598	H		paste	
25	41	42.3	200	Н	VIP CHICK		
56	41	42.3	200	Н	VIP MELGA	_	
27	41	42.3	264	-	SURE HELHP	helicoba	
28	41	42.3	1361	-1		Q91661 xenopus lae	
59	40	41.2	207	٦			
30	40	41.2	238	-	YC53_PORPU	P51202 porphyra pu	
31	40	41.2	385	Н	YFDO_YEAST		
32	40	41.2	488	Н			
33	40	41.2	561	Н	Y423_MYCPN	P75174 mycoplasma	

O26541 methanobact	Q9syq8 arabidopsis	P23579 euglena gra	Q97eg9 clostridium	P47310 mycoplasma				Q20140 caenorhabdi	Q61199 mus musculu	O94404 schizosacch	Q9bxy5 homo sapien
UVRC_METTH	CLV1_ARATH	RPOB_EUGGR	RPOB CLOAB	YO64 MYCGE	DYHB HUMAN	BCP_HELPJ	BCP HELPY	KADI CAEEL	NXP2 MOUSE	YJ3C_SCHPO	CAY2_HUMAN
н,	-	-	-	-	Н	-	-	-	-	ч	7
579	980	1082	1241	1331	4523	152	152	210	244	278	382
41.2	41.2	41.2	41.2	41.2	41.2	40.2	40.2	40.2	40.2	40.2	40.2
04.	40	40	40	40	40	39	39	39	39	39	39
4.1	v.	9	.7	38	39	40	11	12	<b>1</b> 3	14	5

## ALIGNMENTS

	STANDARD; PRT; 668 AA.	i (Rel. 29, Created)	update)	Noncapsid protein NS-1 (Nonstructural protein NS1). NS1.	Luiii.	Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.	:35339;		KOM N.A.	MEDINESSZY/LZB; FULNYGGESZYL/LZB; N. Chen K C Bates B C Jederma M .		localization of a unique sequence possibly responsible for its	on pattern.";	Virology 192:339-345(1993).	-!- FUNCTION: Seems necessary for viral DNA replication.	<ul> <li>-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.</li> </ul>	DOOR Catture is converient It is accommonly a collaboration	between the Swiss Institute of Bioinformatics and the EMBL outstation -	the European Bioinformatics Institute. There are no restrictions on its	on-profit institutions as long as its content is in no way	modified and this statement is not removed. Usage by and for commercial	entities requires a license agreement (See http://www.isb-sib.ch/announce/	email to license@isb-sib.ch).	EMBL) MAIABB : NOT ANNOTATED CDS.	FIR's A442/0; A442/0; A442/0; TITLE TIPLE TO	157: Parvo NS1: 1	Nonstructural protein; Noncapsid protein; DNA replication;		399 406 A	668 AA; 75846 MW; CAE69049F8F86B53 CRC64;	96.9%; Score 94; DB 1; Length 668;	yative 1	
T 1	PAVL3 VNCS PAVL3 P36311.	4 4	15-DEC-1998 (R	Noncapsid prot NS1.	Parvovirus LuIII	Viruses; ssDNA	NCBI_TaxID=35339;	[1]	SEQUENCE FROM N.A.	MEDLINE=9329/126; FUDME Diffoot N Chen K C	"The complete	localization o	encapsidation pattern.";	Virology 192:3	- I - FUNCTION:	-!- SIMILARITY	This curecipo	hetween the S	the European B	use by non-p	modified and t	entities requi	or send an ema	EMBL; MB1888;	FIK; A442/6; A442/6.	Pfam: PF01057:	Nonstructural	ATP-binding.	•	SEQUENCE 668	Query Match	Matches 19; Co	
RESULT	I ON CA		15	O E					ж 2	¥ &	E	RT	RT	RL	ပ္ပ	ខ្ល									ž 6					og G	One	Mat	(

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RESULT 2
VNCS\_MUMIM

ID \_VNCS\_MUMIM STANDARD; PRT; 672 AA.
AC P07300, P10837;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

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ATP-binding.
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                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                    Query Match
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VNCS_PAVHH
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                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed, Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                              autonomous parvovirus, minute virus of mice.";
Nucleic Acids Res. 13:3617-3633(1985).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEIC ACIDE KEB. 11:999-1016/1959.
-1- FUNCTION: Seems necessary for viral DNA replication.
-1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                        MEDLINE-85242059; PubMed-3855242;
Sahli R., McMaster G.K., Hirt B.;
"DNA sequence comparison between two tissue-specific variants of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=83143341; PubMed=6298737;
Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
"The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                 Astell C.R., Gardiner B.M., Tattersall P., "DNA sequence of the lymphotropic variant of minute virus of mic
MVM(i), and comparison with the DNA sequence of the fibrotropic
                        Murine minute virus (strain MVMi) (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=10794;
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created).
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.9%; Score 94; DB 1; Length 672; 95.0%; Pred. No. 2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       597 I -> L (IN REF. 2).
76140 MW; 25F025FB328B4DF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       672 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parvovirus.";
Nucleic Acids Res. 11:999-1018(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X02481; -; NOT_ANNOTATED_CDS.
                                                                                        MEDLINE=86115415; PubMed=3502703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 EVSIKTTLKELVHKRVTSPE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVAIKTTLKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.08;
                                                                                                                                          prototype strain.";
J. Virol. 57:656-669(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 19; Conserv
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                         SEQUENCE FROM N.A.
                                                NCBI_TaxID=10795;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNCS MUMIV
P03134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NCBI_TaxID=10799;
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                                                                                                                                                               EMBL, J02275; AA67109.1; -.
EMBL, VOILIS; CAA24309.1; ALT_INIT.
PIR, A03696; UTVIN.
TRANSFAC; T02375; -.
InterPro; IPR01257; Parvo_NS1.
Fam; PR01057; Parvo_NS1.
Nonetructural protein; Noncapeid protein; DNA replication; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
1-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X01457; CAA25689.1; -.
PIR; A03695; UYPVV1.
InterPro; IPR001257; Parvo NS1.
Pfam; PP01057; Parvo NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.9%; Score 94; DB 1; Length 672; 95.0%; Pred. No. 2e-07;
       and the
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                                                                                                                                                                                                                                                                                                                                                                                    76248 MW; 50298F27662E3C1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).
12F331142F72AA6D CRC64;
between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i
                                                                                                                                                                                                                                                                                                                                                                                                                                   96.9%; Score 94; DB 1; 95.0%; Pred. No. 2e-07;
                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                672 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281 EVSIKTTLKELVHKRVTSPE 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVAIKTILKELVHKRVTSPE 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75993 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 95.0
nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                              406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hamster parvovirus H1,
                                                                                                                                                                                                                                                                                                                                                                                       672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           672 AA;
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Virology 183:195-205(1991).

-I- FUNCTION: Seems necessary for viral DNA replication.

-I- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.

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"Construction and nucleotide sequence analysis of an infectious DNA
"Construction and nucleotide sequence analysis of an infectious DNA
clone of the autonomous parvovirus, mink enteritis virus.";
J. Gen. Virol. 72.867-875 (1991).
-I- FUNCTION: Seems necessary for viral DNA replication.
-I- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                  "Mapping specific functions in the capsid structure of canine
parvovirus and feline panleukopenia virus using infectious plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-91202123; PubMed-2016597;
Kariatsumari T., Horiuchi M., Hama E., Yaguchi K., Ishigurio N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus
NCBI_TaxID=10793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 73; DB 1; Length 668; Pred. No. 0.00051; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76768 MW; 4F8FEA3EE62D2AE7 CRC64;
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I -> V (IN REF. 2).
I -> N (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X55115; CAA38910.1; -.
EMBL; M38246; AAC37927.1; -.
PIR; A36608; UVPVFP.
InterPro; IPR00359; AAA_ATPase.
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo_NS1; I.
J. Gen. Virol. 71:2747-2753 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 EVSIKCTLRDLVSKRVTSPE 301
                                                                                                                                 MEDLINE=91272479; PubMed=1647068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVAIKTTLKELVHKRVTSPE 20
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Best Local Similarity 75.0
Matches 15; Conservative
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443
575
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575
668 AA;
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                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                      Parrish C.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNCS MEVA
                                                                                                                                                                                                                                                                      clones.";
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   REAL STANDARY OF STANDARY SERVICE STANDARY SERVICE SER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hahn W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=193/70;
MEDLINE=91073139; PubMed=2174965;
MEDLINE=91073139; PubMed=2174965;
MARTYN J.C., Davidson B.E., Studdert M.J.;
"Nucleotide sequence of feline panleukopenia virus: comparison with canine parvovirus identifies host-specific differences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
BEDLINE-85265017; PubMed=2991581;
Carlson J., Rushlow K., Maxwell I., Maxwell F., Winston S., Hahn "Cloning and sequence of DNA encoding structural proteins of the autonomous parvovirus feline panleukopenia virus.";
                                                                                                                                                                                                                                                                                                                                                                            Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae, Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.3%; Score 73; DB 1; Length 392; 75.0%; Pred. No. 0.0003; rive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992 (Rel. 21, Created)
1-MAR-1992 (Rel. 21, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
                                                                                                                                                                                              01-JAN-1988 (Rel. 06, Created)
1-JAN-1988 (Rel. 06, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nonstructural protein; Noncapsid protein; DNA replication;

    Virol. 55:574-587(1985).
    FUNCTION: Seems necessary for viral DNA replication.

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392 AA; 43971 MW; B875ADDB4977F616 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                668 AA.
                                                                                                                                    392 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; I.
SMART; SM00382; AAA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVAIKTILKELVHKRVTSPE 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 75.0 les 15; Conservative
                                                                                                                                    STANDARD;
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P24842;
                                                                                                                                                                                                                                                                                                                                       (Fragment)
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SEQUENCE Query Match

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VNCS FPV19
ID VNCS FB
DT O1-MAR.

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Gaps

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282 EVSIKCTLRDLVSKRVTSPE 301

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                                                                                                                                                                                                ö
  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-88062922; PubMed-2824850;
Reed A.P., Jones E.V., Miller T.J.;
"Nucleotide sequence and genome organization of canine parvovirus.";
J. Virol. 62:266-276(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: Seems necessary for viral DNA replication.
-1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                      Canine parvovirus (strain N) (CPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10791;
                                                                                          Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                    75.3%; Score 73; DB 1; Length 668; 75.0%; Pred. No. 0.00051; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.3%; Score 73; DB 1; Length 668; 75.0%; Pred. No. 0.00051;
                                                                                                                                 400 407 ATP (POTENTIAL).
668 AA; 76736 MW; DBD5F9E92113685C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400 407 ATP (POTENTIAL).
668 AA; 76764 MW; DE2CCEA69D2A63A6 CRC64;
                                                                                                                                                                                                                                                                                                                           01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
                                                                                                                                                                                                                                                                                                        668 AA.
entities requires a license agreement (or send an email to license@isb-sib.ch)
                                EMBL; D00765; BAA00662.1; -.
PIR; A38350; UYPVME.
InterPro; IPR001359; AAA ATPase.
InterPro; IPR001257; Parvo_NS1.
Pfam; PP01057; Parvo_NS1; I.
SMART; SM00392; AAA; I.
                                                                                                                                                                                                                                  282 EVSIKCTLRDLVSKRVTSPE 301
                                                                                                                                                                                                                     1 EVAIKTILKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A29962; UYPVCP.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001257; Parvo_NS1.
Pfam; PP01057; Parvo_NS1; I.
SMART; SM00382; AAA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M19296; AAA67459.1; -. EMBL; M38245; AAB02798.1; -.
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                 Local Similarity
tes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parrish C.R.;
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                                                                                                                                                                                                                                                                                                      VNCS PAVCN
P12929;
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SEQUENCE
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SEQUENCE
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Best Local S:
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 367-660 FROM N.A.
MEDLINE=90085785; PubMed=2596019;
Wasudevacharya J., Basak S., Srimivas R.V., Compans R.W.;
Vasudevacharya J., Basak S., Srimivas R.V., Compans R.W.;
"Nucleotide sequence analysis of the capsid genes and the right-hand terminal palindrome of porcine parvovirus, strain NADL-2.";
Virology 173:368-377(1989).
-1- FUNCTION: Seems necessary for viral DNA replication.
-1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE=91021005; PubMed=2219713; Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.; Tasudevacharya J., Basak S., Srinivas R.V., Compans R.W.; Tasudevacharya J., Basak S., Srinivas R.V., Compans R.W.; M.; Tasudevacharya Sequence of an infectious clone of porcine Virology 178:611-616(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G -> R (IN REF. 2).
K -> R (IN REF. 2).
C -> V (IN REF. 2).
TALTOHARFSNTDT -> NLHLTPTPPDSAIRTP (IN
                                                                                                                                                                                                                 Porcine parvovirus (strain NADL-2) (PPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                      Ranz A.I., Manclus J.J., Diaz-Aroca E., Casal J.I.;
"Porcine parvovirus: DNA sequence and genome organization.";
J. Gen. Virol. 70:2541-2553(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.8%; Score 58; DB 1; Length 660; 60.0%; Pred. No. 0.13; ive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REF. 2).
75300 MW; C0B1DF2226A2EF0A CRC64;
VNCS_PAVPN STANDARD; PRT; 660 AA.
P18547; P22965;
01-NOV-1990 (Rel. 16, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1)
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=90010964; PubMed=2794971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D00623; BAA00501.1; -. EMBL; M38367; AAA46920.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M32787; AAA46916.1; -. PIR; A33302; UYPVPP.
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tes 12; Conserv
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Matches
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2; Indels

3; Mismatches

1 EVAIKTTLKELVHKRVTSPE 20

Local Similarity 75.0 les 15; Conservative

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Pfam; PF00311; PEPcase; 1.
non-profit
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Best Local Similarity
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28-FEB-2003
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                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                             those of NADL-2 and field isolates.";
J. Virol. 70:2508-2515(1996).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22084549; PubMed=12089438; Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S., Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.; "50 million years of genomic stasis in endosymbiotic bacteria."; Science 296:2376-2379 (2002).
-! SIMILARITY: STRONG, TO E.COLI YHGI AND H.INFLUENZAE H10433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                                                                                           MEDIINE-90183900; PubMed-8642680;
Bergeron J., Hebert B., Tijssen P.;
"Genome organization of the Kresse strain of porcine parvovirus:
identification of the allotropic determinant and comparison with
                                                                                                 Porcine parvovirus (strain Kresse) (PPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; DB 1; Length 662; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).
B53F76D9F9FBD613 CRC64;
                                   01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ze-FEB-2003 (Rel. 41, Last sequence update)
128-FEB-2003 (Rel. 41, Last annotation update)
139-FEB-2003 (Rel. 41, Last annotation update)
1405525.
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              662 AA.
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                                                                                                                                                                                                                                                                                                                                                     or send an email to license@igb-sib.ch).
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Pfam; PF01057; Parvo NS1; 1.
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Best Local Similarity 60.0%,
-% 12, Conservative
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              STANDARD;
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                                                                                                                           NCBI_TaxID=73487;
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Q8K934;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O + phosphoenolpyruvate + CO(2).
-!- ENZYME REGULATION: By light-reversible phosphorylation.
-!- PATHWAY: Tricarboxylic acid cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Poetsch W., Hermans J., Westhoff P.;
"Multiple cDNAs of phosphoenolpyruvate carboxylase in the C4 dicot
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 192;
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28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Poetsch W.; Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                            Probom; PD002830; NifU C; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 192 AA; 21665 MW; 7C3E41BC59D2FBDC CRC64;
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-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SIMILARITY: Belongs to the PEPCase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 1
Pred. No. 3.3;
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                                                                                                                                                                InterPro; IPR000361; HesB yadR yfhF InterPro; IPR001075; NifU C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
                                                                                                                                  EMBL; AE014127; AAM68067.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EBS Lett. 292:133-136(1991).
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57.9%;
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                                                                                                                                                                                                                                 Pfam; PF01521; HesB-like; Pfam; PF01106; NifU-like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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1; Length 966;

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FLATR
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         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
campanulids, Asterales, Asteraceae, Asteroideae, Tageteae, Flaveria.
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP) it forms oxaloacetate, a four-carbon dicarboxylic acid source for the tricarboxylic acid cycle.
PRINTS, PR00150; PEPCARBXLASE.
PROSITE; PS00393; PEPCASE_2; 1.
PROSITE; PS00781; PEPCASE_1; 1.
Lyase; Carbon dioxide fixation; Allosteric enzyme; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: Tricarboxylic acid cycle. This isozyme is involved in C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0150; PEPCARBXLASE.
PROSITE; PS00393; PEPCASE 2; 1.
PROSITE; PS00781; PEPCASE 1; 1.
Lyase; Carbon dioxide fixation; Allosteric enzyme; Multigene family;
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O + phosphoenolpyruvate + CO(2).

ENZYME REGULATION: By light-reversible phosphorylation (By
                                                                                  Tricarboxylic acid cycle; Phosphorylation; Photosynthesis.
MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tricarboxylic acid cycle; Phosphorylation; Photosynthesis.

MOD RES
11 11 PHOSPHORYLATION (BY SIMILARITY)
ACT SITE 172 BY SIMILARITY.

ACT SITE 600 BY SIMILARITY.

SEQUENCE 966 AA; 110405 MW; 252DB9E9070BC109 CRC64;
                                                                                                                                                                                                                              47.4%; Score 46; DB 1; Length 966; 55.0%; Pred. No. 17; ive 1; Mismatches 8; Indels
                                                                                                                                    172 172 BY SIMILARITY.
600 600 BY SIMILARITY.
966 AA; 110406 MW; 252F7B674BC94F47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28.FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Homotetramer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the PEPCase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 966 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                     135 ESDIEETFKRLVHKLNKSPE 154
                                                                                                                                                                                                                                                                                                                        1 EVAIKTILKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001449; PEPcase.
Pfam; PF00311; PEPcase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, Z25853; CAA81072.1; -. PIR, S37072; S37072.
                                                                                                                                                                                                    Query Match
Best Local Similarity 55.0%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flaveria australasica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 photosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P00864; 1FIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=29716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity)
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CAPP FLAAU

TO Q42730;

DT 01-NOV-1997

DT 01-NOV-1997

DT 01-NOV-1997

DT 28-FEB-2003

DE Phosphoenolp

OS Eukaryota; V C Spermatophyt

OC Gampanulida;

OX NCBI TaxID=2

RN [1]

RA Bauwe H.;

CC -1- FUNCTION

CC -1- FUNCTION

CC -1- SUBCELLU

CC -1- S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Leaf;
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Flaveria trinervia (Clustered yellowtops).
Bukaryota; Viridiplantes; Streptophyte; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Asteroideae; Tageteae; Flaveria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92374996; PubMed=1508152;
Hermans J., Westhoff P.;
Hermans J., Westhoff P.;
Hormologous genes for the C4 isoform of phosphoenolpyruvate
carboxylase in a C3 and a C4 Flaveria species.";
Mol. Gen. Genet. 234:275-284(1992).
-!-FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP)
it forms oxaloacetate, a four-carbon dicarboxylic acid source for
the tricarboxylic acid cycle.
-!- CATALXTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- ENZYME REGULATION: By light-reversible phosphorylation.
--- PATHMAY: Tricarboxylic acid cycle. This isozyme is involved in C4-photosynthesis.
---- SUBUNIT: Homotetramer.
---- SUBCELLIAR LOGATION: Cytoplasmic.
---- TISSUE SPECIFICITY: Mesophyll cells of leaves.
---- SIMILARITY: Belongs to the PEPCase family.
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROBLES, ENGISES, PEPCASE 2; 1.
PROSITE; PS00393; PEPCASE 2; 1.
Lyase; Carbon dioxide fixation; Allosteric enzyme; Multigene family;
Tricarboxylic acid cycle; Phosphorylation; Photosynthesis.
MOD RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 17;
1; Mismatches 8; Indels
                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
1; 61E8A493842E1C1F CRC64;
                                                                                                                                                                                                                                                                                                                     967 AA.
Pred. No. 17;
1; Mismatches
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                                                                                                                                   | |: | | |||| |||
ESDIEETFKRLVHKLNKSPE 154
                                                                                            1 EVAIKTILKELVHKRVTSPE 20
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InterPro; IPRO01449; PEPcase.
PERM, PF00311; PEPcase; I
PRINTS; PR00150; PEPCARBXLASE.
   55.0%;
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1 Similarity 55.0%;
11; Conservative 1
Best_Local Similarity 55.0
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E., Bisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M., Haft D.H., Kolonay J.F., Nelson W.C., Mason T., Tallon L., Gray J., Dewhirst P.E., Tetelin H., Dong H., Galvin J.L., Duncan M.J., Dewhirst F.E., Fraser C.M.;

"Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";

J. Bacteriol. 165:5591-5601(2003)

-!- CATALYTITY: Hydrolysis of terminal non-reducing N-accetyl-D-hexosamine residues in N-acetyl-beta-D-hexosaminides.
                                                                                                                                                                                                                                                                                      Lovatt A., Roberts I.S.; "Cloning and expression in Escherichia coli of the nahA gene from Porphyromonas gingivalis indicates that beta-N-acetylhexosaminidase is an outer-membrane-associated lipoprotein."; Microbiology 140:3399-3406(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BETA-HEXOSAMINIDASE.
N-palmitoyl cysteine (Probable).
S-diacylglycerol cysteine (Probable).
                             01-FEB-1996 (Rel. 33, Created)
10-GCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
Beta-hexosaminidase precursor (EC 31.1.52) (N-acetyl-beta-glucosaminidase) (Beta-GlcNAcase) (Beta-N-acetylhexosaminidase)
                                                                                                                                                   Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anchor (Probable).
-!- SIMILARITY: Belongs to family 20 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Hydrolase; Glycosidase; Signal; Outer membrane; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOASSD2C2FFAD864 CRC64;
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E -> M (IN REF. 1).
LA -> FR (IN REF. 1).
T -> S (IN REF. 1).
G -> A (IN REF. 1).
777 AA
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InterPro; IPR00437; Prok lipoprot_S.
Pfam, PF00728; Glyco hydro 20; 1.
Pfam; PF02838; Glyco hydro 20b; 1.
PRINTS; PR00738; GLHYDRLASE20.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=W83;
MEDLINE=22829867; PubMed=12949112;
                                                                                                                                                                                                                                                                      MEDLINE=95187310; PubMed=7881557;
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 STANDARD;
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265
282
282
575
747
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                       NCBI_TaxID=837;
                                                                                                                                     NAHA OR PG0043
                                                                                                                     (Beta-NAHASE)
 HEXA PORGI
                                                                                                                                                                                                                                                        STRAIN-W83
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Gaps
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 DB 1; Length 777;
                           Indels
Score 45; DB 1
Pred. No. 20;
8; Mismatches
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652 EVGTVSSLEEIMHGKEKITSPE 673
                                                      1 EVAIKTTLKELVH--KRVTSPE 20
Query Match
Best Local Similarity 40.9%;
Matches 9; Conservative
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completed: May 28, 2004, 12:57:41 le :.7.75 secs Search

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P90484 984393 P89514 O71157 O95RCZ O818VZ O9DCL4 O9DCL4 O9CRAJ O9

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mouse parvo
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071159 kilham rat
081918 rat minute
083429 mouse parvo
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084363 felline panl
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                                                                                                                                                                                 1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                              1017041 segs, 315518202 residues
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                                     OM protein - protein search, using sw model
                                                                                                               1 EVAIKTTLKELVHKRVTSPE 20
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O71159
O8JV18
P88899
Q8J429
Q8JV14
Q8JV16
Q84365
Q84363
P89516
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
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Maximum Match 100%
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sp_archeap:*
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sp_organelle:*
sp_phage:*
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Maximum DB seq length: 200000000
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SEQUENCE FROM N.A.

STRAIN=U-Mass;

Jacoby R.O.;

SEQUENCE Query Match

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Noi. Kilham rat virus.

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SEQUENCE FROM N.A.
MEDLINE=9436551; Pubmed=8083985;
Ball-Goodrich L.J., Johnson E.;
Hoolecular characterization of a newly recognized mouse parvovirus.";
J. Virol. 68:6476-6486(1994).
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Mouse parvovirus 1.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBL_TaxID=35340;
                                           Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=12441;
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Brown Cof a Diabetogenic Parvovirus of Rats.";
"Sequence of a Diabetogenic Parvovirus of Rats.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U79033; AAB38326.1; -
Interbro; IRR01257; Parvo NS1.
Pfam; PF01057; Parvo NS1.
SEQUENCE 672 AA; 76056 MW; 0299B36871A0A10A CRC64;
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Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
EMBL, 102469, AAA61405.1. -
InterPro; IRRO01257; Parvo NS1.
Pfam; PF01057; Parvo NS1.
SEQUENCE 672 AA; 76112 MW; 31C6365276727363 CRC64;
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01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
Nonstructural protein 1.
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Matches 19; Conservative
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                                                                 NCBI_TaxID=12441;
                      Kilham rat virus.
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=172385;
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Ball-Goodrich L.J., Leland S.E., Johnson E.A., Paturzo F.X.,
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MEDINES=2212010; PubMed=12124471;
WAN C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.,
"Molecular characterization of three newly recognized rat
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EMBL, AF332882; AAM93275.1; -.

InterPro; IPRO11257; Parvo.NS1.

Pfam; PF01057; Parvo.NS1; 1.

SEQUENCE 672 AA; 76059 MW; 63D8B9EBF99E07B3 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Nonstructural protein (Fragment).
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InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
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J. Virol. 72:3289-3299(1998).
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RESULT 3
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NCBI_TaxID=172386;
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                            MEDINE=22120170; PubMed=12124471;
Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
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Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
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Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                      parvoviruses.",
J. Gen. Virol. 83.2075-2083(2002).
EMBL; AF321230; AAM93272.1; -.
Interbro; IRR01257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SEQUENCE 672 AA; 75987 MW; 22B4611C20CDB6E9 CRC64;
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J. Gen. Virol. 83:2075-2083(2002).

EMBL; AA932884; AAM93279.1; -.
InterPro; IPR01257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SEQUENCE 672 AA; 75988 MW; 52DF6549349CF3FD CRC64;
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J. Gen. Virol. 83:2075-2083(2002).
EMBL; AF332883; AAM93277.1; -.
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Matches 19; Conservative
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Rat minute virus 1b.
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SEQUENCE FROM N.A.
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STRAIN=MVM(p);
STRAIN=MVM(p);
ABDLINE=83143341; PubMed=6298737;
Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
"The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MVM(p);
MEDLINE=86115415; PubMed=3502703;
MEDLINE=86115415; PubMed=3502703;
Astcall C.R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mic MVM(1), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10794;
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InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; 1.
SEQUENCE 672 AA; 76201 MW; C2F1A71F6EF449A6 CRC64;
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Pfam; PF01057; Parvo NSI; 1.
SEQUENCE 721 AA; 81896 MW; 18391758E42F0DCF CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Nonstructural protein.
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Nucleic Acids Res. 11:999-1018(1983)
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"Evolutinary pattern of feline panleukopeina virus differs that of
canine parvovirus.";
                                                                                                                                                               STRAIN=1ymphotropic variant,
MEDLINE=66115415; PubMed=1502703;
Astell C.R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mic
MVM(1), and comparison with the DNA sequence of the fibrotropic
Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10786;
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EMBL, AB000062; BAA19023.1; -.
GO; GO:0000166; F:nucleotide binding; IEA.
InterPro; IPR003593; AAA AFPase.
InterPro; IPR001257; Parvo NS1.
EFGan; PF01057; Parvo NS1.
SMART; SM00382; AAA; 1.
SEQUENCE 668 AA; 7:6755 MW; 37ABDFD347017F52 CRC64;
                                                                                                                                                                                                                                                                                                                                            prototype strain.";
J. Virol. 570:656-669(1986).
EMBL; M12032; AAA69566.1; -.
PIN; A23009; UTVOVIM.
InterPro; IPR001257; Parvo NSI.
Pfam; PF01057; Parvo NSI; I.
SEQUENCE 721 AA; 81863 MW; 9FD29C327C7F4BBF CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                     SEQUENCE FROM N.A.
                                                                 NCBI_TaxID=10794;
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01-MAY-1997
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P89516
P89516
AC P89511
AC P8951
DT 01-MA
DT 01
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=10786;
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Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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                                             of canine parvovirus.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AB000015; BAA19018.1;
GO; GO:000166; F:nucleotide binding; IEA.
InterPro; IPR001559; AAA_ArPase.
InterPro; IPR0157; Parvo NS1.
Pfam; PF01057; Parvo NS1.
Fram; PF01057; Parvo NS1; I.
SMART; SM00382; AAA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Horiuchi M.;
Horiuchi M.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB000069; BAA19020.1; -.
EMBL; AB0000663; BAA19024.1; -.
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668 AA; 76769 MW; OECAFEGBF62ASDE0 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Nonstructural protein 1.
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01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GO; GO:000166; F:nuclectide binding; IEA.
InterPro; IPR003593; AAA ATBSE.
InterPro; IPR001257; Parvo_NS1.
SMART; SR00382; AAA; I.
Nonstructural protein.
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                                                                                                                                                                                                                                                                                                                                    Local Similarity 75.0 es 15; Conservative
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Horiuchi M.;
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Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10786;
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                                                          E SUBMITTER ('JAN-1997) to the EMBL/GenBank/DDBJ databases.

R EMBL; AB000065; BAA19028-1; --

R EMBL; AB000065; BAA19028-1; --

R GO; GO:0001065; Erucleotide binding; IEA.

R GO; GO:000106; F:nucleotide binding; IEA.

R InterPro; IPR001557; PAA_ATPasse.

R InterPro; IPR001557; PATO NS1.

R SMART; SMO0382; AAA, 1.

NOMSTRUCURAL PROTECHI.

NOMSTRUCURAL PROTECHI.

SEQUENCE 668 AA; 76755 MW; 008CED50178833EF CRC64;
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AB0000158; BAA19011.1; --
GO; 60:0000166; F:nuclectide binding; IEA.
InterPro; IPR00159; AAA ATPase.
InterPro; IPR01257; Parvo NS1.
Fam: PF01057; PAN; I.
SMART; SM00382; AAA; I.
SEQUENCE 668 AA; 76743 MW; 84A210104D9D5788 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Search completed: May 28, 2004, 13:00:02 Job time: 33 secs

282 EVSIKCTLRDLVSKRVTSPE 301

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Sequence 745,

7151, Ap 15071, Ap 11, Appl 11, Appl 16, Appl 15, Appl 15, Appl 16, Appl 6, Appl 7, Appl 7, Appl 8, Appl 8, Appl 12, Appl 13, Appl 14, Appl 14, Appl 15, Appl 16, Appl 16, Appl 16, Appl 16, Appl 17, Appl 17, Appl 18, Appl 19, Appl 18, Appl 18, Appl 18, Appl 18, Appl 18, Appl 18, Appl 19, Appl 18, App

Perfect score:

Sequence:

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Run

Scoring table:

Searched:

Database

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JOHNSTON INCOMENTATION

APPLICANT: Caplinski, Kevin

APPLICANT: Caplinski, Kevin

APPLICANT: Caplinski, Kevin

APPLICANT: Caplinski, Kevin

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 60.1.1-65N

CURRENT APPLICATION NUMBER: US/09/359,268A

CURRENT APPLICATION NUMBER: 05/093,685

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 26
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APPLICANT: Christensen, Tove
APPLICANT: Christensen, Tove
APPLICANT: Lehmbeck, Jan
TITLE OF INVENTION: A Fungus Wherein The area, pepC and/or
TITLE OF INVENTION: pepE Genes Have Been Inactivated
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60134520 No. 6013452disk of No. 6013452th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
                                            Sequence 7151
Sequence 1003
Sequence 11,
Sequence 14,
Sequence 16,
Sequence 16,
Sequence 15,
Sequence 15,
Sequence 15,
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Sequence 5997
Sequence 66,
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44.8%; Score 43.5; DB 4; Length 472;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 14; Conservative 2; Mismatches 3; Indels
                                            US-09-543-681A-7151
US-09-134-001C-5071
US-09-198-452A-1003
US-09-080-983-11
US-09-360-1463A-14
US-09-360-197-16
US-09-650-656-15
US-09-650-656-15
US-08-483-101-14
US-08-483-101-14
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US-09-252-991A-23671
US-09-543-681A-5997
-09-198-452A-745
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US-09-614-480-2
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GENERAL INFORMATION:
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Patent No. 6013452
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US-09-359-268A-26
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US-09-079-415-2
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Sequence 6581, Ap
Sequence 4, Appli
Sequence 4, Appli
Sequence 247, App
Sequence 247, App
Sequence 6, Appli
Sequence 12030, Ap
Sequence 100, App
Sequence 110, App
Sequence 11, Appli
Sequence 6712, Ap
Sequence 611, Appli
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5150, Ap
5739, Ap
4162, Ap
5738, Ap
5746, Ap
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                                                                                                                                                                       May 28, 2004, 12:53:44 ; Search time 13.5 Seconds (without alignments) 76.483 Million cell updates/sec
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(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-079-415-2
US-09-079-415-2
US-08-799-138-4
US-08-392-362-4
US-08-473-553A-4
US-08-473-553A-6
US-08-473-553A-6
US-08-473-553A-6
US-08-473-553A-6
US-08-473-553A-6
US-08-489-039A-12030
US-08-680-560-11
US-09-198-452A-801
US-09-198-452A-801
US-09-198-452A-801
US-09-198-452A-801
US-09-198-452A-801
US-09-198-452A-801
US-09-198-452A-801
US-09-198-452A-801
US-09-107-532A-5724
US-09-107-532A-5724
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US-09-107-532A-5053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                             1 EVAIKTTLKELVHKRVTSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                   US-10-069-056-5
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Match Length
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Gaps

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Result No.

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46.7%; Pred. No. 1.6e+02;
tive 5; Mismatches 3; Indels
                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/799,138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09392362
Patent No. 6248868
GENERAL INFORMATION:
APPLICANT: Verma, Desh Pal
TITLE OF INVENTION: PHRAGMOPLASTIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CALFEE, HALTER & GRISWOLD
STREET: 800 SUPERIOR AVENUE
CONTY: CLEVELAND
                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLRICK, WARY E
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00139
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: GOLRICK, MARY E
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00139
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/799,138
                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (216) 622-8458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |: : ||:|||| ::
428 AVHSLLKDLVHKAIS 442
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                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 610 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                         COMPUTER READABLE FORM:
        CLEVELAND
                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OHIO
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                                                                      44114
                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: CLI
STATE: OF
COUNTRY:
                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-799-138-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6583, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: UNMER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.3%; Score 41; DB 4; Length 198; 56.2%; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,415
FILING DATE: 14-MAY-1998
CLASSIFICATION: NUMBER: 36,993
REGISTRATION NUMBER: 36,993
REGISTRATION NUMBER: 36,993
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 4657.204-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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Patent No. 5994053
GENERAL INFORMATION:
APPLICANT: Verma, Desh Pal
ITILE OF INVENTION: PHRAGMOPLASTIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSE:
ADDRESSEE: CALFEE, HALTER & GRISWOLD
STREET: 800 SUPERIOR AVENUE
                                                                                                                                                                                                                                                                                                                TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-079-415-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
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292 IALATTLAELINKEI 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 56.2
Matches 9; Conservative
COMPUTER READABLE FORM MEDIUM TYPE: Disket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -09-543-681A-6583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-543-681A-6583
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US-08-799-138-4
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OPERATING SYSTEM:
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STRANDEDNESS: unl
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: un
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                                                                                                                Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TSONGAIG, Bliana
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: VIRULENCE AND USES THEREOF
FILE REFERENCE: 00708/341002
CURRENT APPLICATION NUMBER: US/09/199,637A
PRIOR PILLING DATE: 1999-11-25
PRIOR PILLING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FASTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 4; Length 177; Pred. No. 66;
                                                                                                                                                       3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herber
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                Score 41; DB 3; I
Pred. No. 1.6e+02;
                                                                                                                                                       5: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                              Sequence 247, Application US/09199637A Patent No. 6355411 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      Ausubel, Frederick
Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08473553A Patent No. 5859338 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                               |::||:||:|
428 AVHSLLKDLVHKAIS 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                             3 AIKTTLKELVHKRVT 17
LENGTH: 610 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 LKELVHKRVTSPB 20
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18 IKHLAHRELTTPE 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States 2IP: 94111-4187
                            / TOPOLOGY: linear
// MOLECULE TYPE: protein
US-09-392-362-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
                                                                                                                                                                                                                                                                                                            US-09-199-637A-247
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US-08-473-553A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 247
LENGTH: 177
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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CITY: San Francisco
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/473,553A
FILING PATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08473553A
Patent No. 585938
GENERAL INFORMATION:
APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
               SOFTWARE:
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
US/08/473,553A
FILING DATE:
O6-JUN-1995
CLASSIFICATION:
800
ATTORNEY/AGENT INFORMATION:
NAME: $11va, Robin M.
REGISTRATION NUMBER: 38,304
REFRENCE/DOCKET NUMBER: 3-60886/RFT/RMS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 41.2%; Score 40; DB 2; Best Local Similarity 35.0%; Pred. No. 1e+02; Matches 7; Conservative 5; Mismatches
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TELECOMMUNICATION INFORMATION:
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 EAAARPTMREVVHMLTNPPK 274
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                                                                                                                                                                                                                                                                    TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 980 amino acids
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 282 amino acids
                                                                                                                                                                                                                                                                                      TELEFAX: (415) 398-324
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER:SETICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-473-553A-4
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APPLICANT: Steinert, Peter M.
APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyu
APPLICANT: Chung, Soo-Il
APPLICANT: Park, Sang-Chul
APPLICANT: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
                                                                                                                                                                                                                                                                                         Query Match
40.7%; Score 39.5; DB 4; Length 424;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 2; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/056,200
FILING DATE: 30-APR-1993
     CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342 EEQ ID NO 12030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 100, Application US/08056200
Patent No. 5616500
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                146 EVPLLAVISELVH-RYRSPE 164
                                                                                                                                                                                                                                                                                                                                                                                              1 EVAIKTILKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISCRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIHOS
TELEPONON: (714) 760-0404
TELEPRAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 100: SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
                                                                                                                                                                                 TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 KTTLKELVHKRVTS 18
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Best Local Similarity 57.1
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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PREEDE NO. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
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                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Meserowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 1
CORRESPONDENCE 11
CORRESPONDENCE Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embacadero Center, Suite 3400
CITY: San Francisco
                                                                          Query Match
41.2%; Score 40; DB 2; Length 980;
Best Local Similarity 35.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 5; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIN Release #1.0, Version #1.30
SOFTWARE: PatentIN RAPELCATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-UNW-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: S11a, Robin M.
REGISTRATION NUMBER: 38,304
REPRENCE/DOKET NUMBER: 38,304
REPRENCE/OKET NUMBER: A-60886/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
TEMPRORMATION POR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08473553A Patent No. 5859338 GENERAL INFORMATION:
                                                                                                                                                                                                                 | | : |::|:|
953 EAARPTMREVVHMLTNPPK 972
                                                                                                                                                                                 1 EVAIKTILKELVHKRVTSPE 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States ZIP: 94111-4187
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; MOLECULE TYPE: protein US-08-473-553A-6
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Best Local Similarity
Matches 7; Conserva
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GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI)

TITLE OF INVENTION: UDAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US (90) 543, 681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 6712
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Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
APPLICANT: Griffais, R.
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT PAPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
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Pred. No. 1.6e+02;
4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                  Score 39; DB 3; Length 151;
Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6712, Application US/09543681A
Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVAIKTILKELVHKRVTSP 19
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ORGANISM: Chlamydia pneumoniae
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Best Local Similarity 52.6%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Gallus gallus
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US-09-543-681A-6712
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US-09-198-452A-801
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                                                                                                                                                                                                                                                                          APPLICANT: Steinert, Peter M.
APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyu
APPLICANT: Chung, Soo-11
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATE: 14-FEB-1997

CLASSIFICATION: 424

FILING DATE: 30-APR-1993

ATTORNEY AGENT INFORMATION:
NAME: Fedrick, Michael F.

REGISTRATION NUMBER: 36,799

REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 2
Pred. No. 23;
2; Mismatches
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TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176(5091
CURRENT APPLICATION NUMBER: US/08/680,506C
                                                                                                                                                                                  Sequence 100, Application US/08800644
Patent No. 5958752
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
      29 KKELKELIQKELTS 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 KTTLKELVHKRVTS 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 44 amino acids
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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US-08-800-644-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                                                                                                            US-08-800-644-100
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US-08-680-506-11
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                                                                                                                             RESULT 12
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Gaps

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Search completed: May 28, 2004, 13:02:03 Job time : 14.5 secs

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May 28, 2004, 12:57:09; Search time 34.75 Seconds (without alignments) 160.719 Million cell updates/sec
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| Cgn2 6/ptodata/1/pubpaa/US06 PUBW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*
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| Cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US09 NEW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US108 PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US60 NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1151071 seqs, 279249464 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                               OM protein - protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	r	202680,	318, App	309, App	470, App	76, Appl	1830, Ap	53696, A	59186, A	62723, A	6689, Ap	6690, Ap	174400,	254410,		
	Description	Seguence 202680,	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence
SUMMARIES		US-10-424-599-202680	S-10-043-487-318	S-10-043-487-309	S-10-177-293-470	S-10-092-900A-76	5-10-369-493-1830	US-10-282-122A-53696	S-10-425-114-59186	5-10-425-114-62723	S-10-369-493-6689	S-10-369-493-6690	S-10-424-599-174400	S-10-424-599-254410	US-10-034-934-116	S-10-425-114-62231
	B ID	12 U	14 U	14 U	14 U	12 U	15 U	12 U	12 U	12 U	15 U	15 U	12 U	12 U	14 U	12 U
	* Query Watch Length DB	94	548	698	2541	2545	2231	66	594	594	1023	1023	53	63	99	262
	& Query Match	50.5	46.4	46.4	46.4	45.4	44.8	44.3	44.3	44.3	44.3	44.3	43.3	43.3	43.3	43.3
	Score	49	45	45	45	44	43.5	43	43	43	43	43	42	42	42	42
	Result No.		7	m	4	ហ	9	7	80	σ	10	11	12	13	14	15

369,	Seguence 2145, Ap	Sequence 2650, Ap	Sequence 9876, Ap	Sequence 155727,	Sequence 960, App	Sequence 282637,	Sequence 282638,	Sequence 7847, Ap		Sequence 247, App	Sequence 162905,		Sequence 62371, A	Seguence 64861, A	Sequence 1380, Ap	Sequence 62984, A	Sequence 8, Appli	Sequence 7237, Ap	Sequence 65307, A		Sequence 65699, A	8, 7	3	164,	5195		Sequence 13941, A	Sequence 59506, A
2 US-10-363-616-369	5 US-IU-369-493-2145 2 HG-10-406-6868-85	5 US-10-264-237-2650	4 US-10-156-761-9876	2 US-10-424-599-155727	US-09-764-864-960	2 US-10-424-599-282637	2 US-10-424-599-282638	4 US-10-032-585-7847	2 US-10-424-599-180939	0 US-09-975-719-247	2 US-10-424-599-162905	2 US-10-424-599-253310	2 US-10-282-122A-62371	2 US-10-282-122A-64861	1 US-09-833-245-1380	2 US-10-425-114-62984	US-09-945-249-8	4 US-10-032-585-7237	2 US-10-425-114-65307	2 US-10-282-122A-65444	2 US-10-282-122A-65699	4 US-10-276-629-8			2 US-10-282-122A-51957		5 US-10-369-493-13941	2 US-10-282-122A-59506
361 1	1 /111	186 1	356 1	610 1	935 9	181 1	240 1	474 1	59 1	177 1	191 1	202 1	207 1	207 1	254 1	329 1	384 9	397 1	517 1	591 1	591 1	591 1	591 1	591 1	1241 1	1331 1	336 1	400 1
2 43.3	4 4 4 5 . 5 A 4 5 . 5 A	42.3		41 42.3	41 42.3	4	4	4	40 41.2	40 41.2	40 41.2	40 41.2	40 41.2	40 41.2	40 41.2	40 41.2	40 41.2	40 41.2	40 41.2	40 41.2	40 41.2	40 41.2	40 41.2	40 41.2	40 41.2	40 41.2	.5	1.5 40.7
16	18 41	19 4	20	21	22	23 40	24 40	25 40	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44 39	45 39

## ALIGNMENTS

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US-10-44-599-202680
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US-10-42-59-202680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Clone ID: PAT_MRT3847_25044C.1.pep
US-10-424-599-202680
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Pred. No. 3.2;
2; Mismatches 3;
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Sequence 318, Application US/10043487

Publication No. US20030055220A1

GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
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Best Local Similarity 64.3%;
Matches 9; Conservative
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31 TLDEMVHKRTLSPD 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
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APPLICANT: Pusztai, Lajos
APPLICANT: Meric, Funda
APPLICANT: Sahin, Ayesqul
APPLICANT: Mils, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
FILE REPRENDE: MRI-038
FILE REPRENDE: MRI-038
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Pred. No. 5.1e+02;
3; Mismatches 5; Indels
                                                                                                                                                                                                            CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SEQ ID NO 470
LENGTH: 2541
                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/177,293 CURRENT FILING DATE: 2002-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 76, Application US/10092900A
Publication No. US20040043382A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Taupler Jr., Raymond J.
APPLICANT: Pena, Carol E.A.
APPLICANT: Li
APPLICANT: Carbusen, Bryan D.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || |::|:| ||||
1863 AIAVTVQEMVTKSNTSPE 1880
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Fernandes, Elma R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.48;
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Catterton, Elina
Leite, Mario W.
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Gangolli, Esha A.
Vernet, Corine A.M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Casman, Stacie J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malyankar, Uriel
Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.63
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-177-293-470
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US-10-092-900A-76
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TITLE OF INVENTION: Protein-protein interactions between Shigella Flexmeri polypeptid
TITLE OF INVENTION: mammalian polypeptides
FILE REFERENCE: B4778A
CURRENT APPLICATION NUMBER: US/10/043,487
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/261,130
PRIOR APPLICATION NUMBER: US 60/261,130
NUMBER OF SEQ ID NOS: 561
SOFTWARE: Patentin version 3.1
                TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptid
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                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 14; Length 548;
Pred. No. 97;
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     46.4%; Score 45; DB 14; Length 698;
1 Similarity 55.6%; Pred. No. 1.3e+02;
10; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                         FILE REFERENCE: B4778 manuscrient polypopolical current APPLICATION NUMBER: US/10/043,487 CURRENT FILING DATE: 2002-04.30 PRIOR APPLICATION NUMBER: US 60/261,130 PRIOR FILING DATE: 2001-01-12 NUMBER OF SEQ ID NOS: 561 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-10-043-487-309
US-10-043-487-309
Sequence 309, Application US/10043487
Publication No. US20030055220A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: HYBRIGENICS
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Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: CALORY, KAREN
APPLICANT: Zhao, Xumei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || |:|:| | ||||
|159 AIAVTVQEMVTKSNTSPE 176
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Best Local Similarity 55.6%;
Matches 10; Conservative
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Kamatkar, Shubhangi
Mertens, Maureen
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Monahan, John
Meyers, Rachel E.
                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Shigella Flexneri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Shigella Flexneri
US-10-043-487-309
Pierre, LEGRAIN
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Wang, Youzhen
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     US-10-043-487-318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 309
LENGTH: 698
TYPE: PRT
                                                                                                                                                                                                                        SEQ ID NO 318
LENGTH: 548
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APPLICANT:
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PRIOR FILING DATE: 2003-02-20
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-23
PRIOR PELLING DATE: 2000-11-27
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PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2001-12-22
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-06
PRIOR PELLING DATE: 2001-02-16
PRIOR PELLING DATE: 2001-02-06
PRIOR PELLING DATE: 2001-03-06
PRIOR PELLING DATE: 2001-03-06
PRIOR PELLING DATE: 2000-03
PRIOR PELLING DATE: 2000-03
PRIOR PELLING DATE: 2000-03
PRIOR PELL
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION UNMER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

44.3%; Score 43; DB

Best Local Similarity 44.4%; Pred. No. 31;

Matches 8; Conservative 7; Mismatches
                             1450 VAIXDLTLEELVDKRIGERNYEIRTDPE 1477
                                                                                                                                                                                                                                                                                 Sequence 53696, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 59186, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Cornyebacterium diptheriae
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58 SIKTTMREDVVEQILTPE 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                               JS-10-282-122A-53696
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APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Bugges, Catherine E.
TITLE OF INVENTION: No. US200043382Alel Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: No. US200043382Alel Proteins and Nucleic Acids Encoding Same
FILE PERFERNER: 21402-290C
CURRENT APPLICATION NUMBER: US6N 60/274,322
FRIOR PELLON NUMBER: USSN 60/274,322
FRIOR PELLON NUMBER: USSN 60/283,675
FRIOR PELLON NUMBER: USSN 60/283,675
FRIOR PELLON NUMBER: USSN 60/274,281
FRIOR PELLON NUMBER: USSN 60/274,281
FRIOR APPLICATION NUMBER: USSN 60/274,281
FRIOR APPLICATION NUMBER: USSN 60/274,191
FRIOR PELLON NUMBER: USSN 60/274,191
FRIOR PELLON NUMBER: USSN 60/274,191
FRIOR PELLON NUMBER: USSN 60/279,995
FRIOR APPLICATION NUMBER: USSN 60/279,995
FRIOR PELLON NUMBER: USSN 60/279,995
FRIOR APPLICATION NUMBER: USSN 60/279,995
FRIOR PELLON NUMBER: USSN 60/279,995
FRIOR PELLON NUMBER: USSN 60/289,899
FRIOR PELLON NUMBER: USSN 60/289,899
FRIOR FILLING DATE: 2001-04-30
FRIOR PELLON NUMBER: USSN 60/289,7424
FRIOR FILLING DATE: 2001-04-30
FRIOR PELLON NUMBER: USSN 60/289,7424
FRIOR FILLING DATE: 2001-04-30
FRIOR FILLING DATE: 2001-
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Sequence 1830, Application US/10369493

Sequence 1830, Application US/10369493

GENERAL INFORMATION:
APPLICANT: Coo, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED ROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28

PRIOR PRILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 1830
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Pred. No. 7.8e+02;
2; Mismatches 3; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
45.4%; Score 44; DB 12; Length 2545;
Best Local Similarity 50.0%; Pred. No. 7.5e+02;
Matches 9; Conservative 4; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 5.
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; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || | :|:: | ||:||
1867 AIAVTAQEMMTKSVTNPE 1884
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Best Local Similarity 50.0%;
Matches 14; Conservative
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2 VAIK-TTLKELVHKRV------TSPE 20

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US-10-424-599-174400
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LENGTH: 29
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53113)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 73128
SEQ ID NOS: 73128
TYPE: ...
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| Publication No. US20030233675A1
| GENERAL INFORMATION:
| APPLICANT: Gao, Yongwei
| APPLICANT: Hinkle, Gregory J.
| APPLICANT: Glater, Steven C.
| APPLICANT: Glater, Xianfeng
| TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
| TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
| TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
| TITLE OF INVENTION: US/10/369,493
| CURRENT APPLICATION NUMBER: US/10/369,493
| CURRENT FILING DATE: 2003-02-28
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FITLE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 59186
LENGTH: 594
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                                                                                                                                                                                                                                                                                                                                            Length 594;
                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
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                                                                                                                                                                                                                                                                                                                                       Score 43; DB 12;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: 700377412_FLI.pep
US-10-425-114-59186
                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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196 VAIKTGIQAFLHPSVTIP 213
                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAIKTILKELVHKRVTSP 19
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Best Local Similarity
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Matches 9, Conserv
                                                                                                                                                                                                                            ORGANISM: Zea mays
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ORGANISM: Zea mays
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US-10-369-493-6689
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Sequence 174400, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Abou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: MATH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6690
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                                                                                                                                                                                                                                                    44.3%; Score 43; DB 15; Length 1023; 60.0%; Pred. No. 4e+02; tive 2; Mismatches 4; Indels
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     60/360,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6690, Application US/10369493
Publication No. US20030233675A1
                                                                                                                                          TYPE: PRT
ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                        674 VKNKLKELVEKKKTS 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               674 VKNKLKELVEKKKTS 688
PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 6689 LENGTH: 1023
                                                                                                                                                                                                                                                                                                                                                                    4 IKTTLKELVHKRVTS 18
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                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.05
Matches 9; Conservative
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Matches 9, Conservative
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ORGANISM: Glycine max
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Sceen, Steven E
APPLICANT: Sceen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plant and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53315) B
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 62231
LENGTH: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 43.3%; Score 42; DB 12; Length 26 Best Local Similarity 40.0%; Pred. No. 1.3e+02; Antches 6; Conservative 7; Mismatches 2; Indels
Indels
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US-10-425-114-62231
5;
Mismatches
                                                                                                                                                                                              Sequence 62231, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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Job time : 35.75 secs
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                                        2 VAIKTTLKELVHKRVTSP 19 | :| | | | | | ::: | | 21 VYLKTNLKEMENRKTFSP 38
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172 LSIRRTARKLIHKRI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VAIKTILKELVHKRV 16
8; Conservative
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FEATURE:
Matches
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                                                                                                                                                                                                                                                       Sequence 254410, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21 (5323.8)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 254410
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Publication No. US20030068624A1

GENERAL INFORMATION:
APPLICANT: Recipon, Herve
APPLICANT: Chen, Yongming
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENTION: Genes and Proteins
FILE REFERENCE: DEX-0245
CURRENT APPLICATION NUMBER: US/10/034,934
CURRENT FILING DATE: 2000-11-26
PRIOR APPLICATION NUMBER: 60/252,055
PRIOR PELING DATE: 2000-11-2
PRIOR FILING DATE: 2000-11-2
NUMBER OF SEQ ID NOS: 142
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 116
                                                                 Gaps
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                Query Match 43.3%; Score 42; DB 12; Length 29; Best Local Similarity 44.4%; Pred. No. 12; Matches 8; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_71756C.1.pep
US-10-424-599-254410
                                                                                                         2 VAIKTTLKELVHKRVTSP 19
                                                                                                                                      10 IRIKTRCYPLIHKOVSYP 27
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; ORGANISM: Homo sapiens
US-10-034-934-116
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Best Local Similarity
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GenCore version 5.1.6
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2, 2004, 15:24:48; Search time 652 Seconds (without alignments) 3988.623 Million cell updates/sec OM nucleic - nucleic search, using sw model June Run on:

1 acaagagcctgcagaatttt......atgttaaagtttgccatgct 60 US-10-069-056-7 60 Title: Perfect score: Sequence:

3470272 seqs, 21671516995 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

6940544 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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DI DI	AX137742 AX137742 AX137736 AX137736 AX137737 AX137737 AX137751 PAMVM2 PAMVM2 MVM42256 MVM34255 MVM34256 MVM34256 MVM34256 MVM34256 PAMSERQ PVRBBWOR AF317513 AF036711 AF32884 AF036711 AF332884 AF036710 AF036710 AF332893 AF036710 AF332893 AF	ALIGNMENTS 60 bp DNA
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Mice minute virus Mice minute virus Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus. AX137742.1 GI:14273915 VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL

Nueesch,J. and Rommelaere,J.
Parvovirus ns1 variants
Parvovirus 181 1077260-4.
Patent: EP 1077260-4.
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts

PAT 30-MAY-2001

linear

FEATURES

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NTVLPHGPASTGKS I AQA AQA VGNYGCYNAANVNPPRNDCTNKNLI WVEEAĞNFGQ
OVNOFKA I CSGQTTR I DQKGKGSKQI EPTPVIMTTNENI TYVR I GCEERPEHTOPI RD
RMAI HILTHTLEGDFGLYDKRWPWI I CAWLVKNYGYQSTWASYCAKWGKVPDWSENWAE
PKVPPTPI NILLGSARS PFTTPKSTPLSQNYALTPLASDILEDLALLEPWSTPNTPVAGTAE
TQNTGEAGSKACQDGQLSPTWSEI EEDLRACFGAEPLKKDFSEPLNLD
1081 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 1140
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NSYKKELOEDELKSLORGAETTWDOSEDMEWETTVDEMTKKOVPIPDSLVKKCLPEVL
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QTKKEVSIKTTLKELVHKRVTSPEDWMMQPDSYIEMMAQPGGENLLKNTLEICTLTL
ARTKTAFDLILEKAETSKLTNFSLPDTRTCRIFAFHGMNYVKVCHAICCVLNRQGGKR
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Parvovirus ns1 variants
Patent: EP 1077260-A 4 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts (DE)
                                                                                                                                                                                                                                                                                                                                                                                                 Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts (\mathrm{DE})
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Viruses; ssDNA viruses; Parvoviridae; Parvovirus
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    /note="unnamed protein product"

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db_xref="GI:14273910"
db_xref="REMTREMBL:CAC39989"
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/organism="Mice minute virus"
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/db_xref="taxon:10794"
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Patent: EP 1077260-A 1 21-FEB-2001;
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Sequence 1 from Patent BP1077260.
AX137736
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AX137739
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RAMNIHLTHTLEGDFGLFVDVREWPHPIARDANLVKROYOSTVASZYCKKWGKVPDWSEKWAE
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TQNTGRAGSKACQDGQLSPTWSEIEBDLARCFGARPLKKDFSEPLNLD
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Patent: EP 1077260-A 8 21-FRB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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                                                                                         /mol_type="unassigned DNA"
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I Similarity 100.0%; Pred. No. 5.6e-10;
60; Conservative 0; Mismatches 0;
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Sequence 8 from Patent EP1077260.
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Matches
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                         RESULT 6
AX137751
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PAMVM2
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                                                                                                                                                                                                                                                                                     CNVQLTPAER I KLREI AEDNEWYTLLTYKHKQTKKDŸT KCVLFGNMI AYYFLTKKKI S
TSPERDGGYFLSEDSGWKTNFLKEGERHLVSKLYTDDNR PETYBTTYTTAQETKRGRI
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ARTKTAFDL I LEKAETSKLTNFSLEPDTRTCR I FAFHGWYVKVCHAI CCVLNRQGGKR
NTVLFHGPASTGKS I I AQAI AQAVGNVGCYNAANVNFPFNDCTNKNL I WVEBAGNFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAVLFHGPASTGKS I JAQA JAQAVGNVGCYNAANVNFPFNDCTNKNL I WVEEAĞNFGQ
QVJOPKAL I GSGQTI BI DQKGKGSKQI EPTPVI MITTNBI I TYVR I GCEBR PEHTQPI RD
RMLN I HLTHTL BGD FGL VOKBWPWI I CAML VKNGYQSTWASY CAKWGKVPDWSENWAE
PKVPP PI NILLGSARSP FTT PKSTPL GQNYALTPLASDLEDLALLEPWSTPNTPVAGTAE
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RMLNIHLTHTLPGDFGLVDKNEWPMICAWLVKNGYQSTWASYCAKWGKVPDWSENWAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKVPTPINLLGSARSPFTTPKSTPLSONYALTPLASDLEDLALEPWSTPNTPVAGTAE
TONTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
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SPRROGGYPTESDSGWRTNFKERGERHLYNSKYTDDNREBTYETTVTAĞETKRGRI
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ARTKTAFDLILEKAETSKLTNFSLPDTRTCRIPAFHGMNYVKVCHAICCVLNRQGGKR
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NTKN1FPGDVNWFVQHEWGKDQGWHCHVL1GGKDFSQAQGKWWRRQLNVYWSRWLVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nueesch,J. and Rommelaere,J.
Barvovints ns1 variants
Patent: EP 1077260-A 12 21-FEB-2001;
Detentsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
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Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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Pred. No. 1.7e-09;
0; Mismatches 1; Indels 0:
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                                                 'note="Parvovirus NS1 variant"
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    .2019
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    /db_xref="taxon:10794"

/mol_type="unassigned DNA"
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                                                                                                                          /codon start=1
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                                                                            .2019
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Best Local Similarity
Matches 59; Conserv
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ACCESSION
VERSION
KEYWORDS
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TITLE
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AX137747
LOCUS
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SOURCE

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QVNQFKA I CSGQA I I I DQKGKGSKQI EPTPVI MTTNRIN I TVR I GCEBREHTYOP I RD
MAIN IHLITHTHGDFGLUVKNEWPM I CAMLVKNGYQSTWASYCAKWGKVPDWSENWAE
PKVPTP I NILIGSARSPETTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAE
TQNTGEAGSKACQDGQLSPTWSE I BEDLRACFGAEPLKKD FSEPLNLD"
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TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARTKTAFDLILEKAETSKLTNFSLPDTRTCRIFAFHGWNYVKVCHAICCVLNRQGGKR
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Mice minute virus
Mice minute virus
Viruses; seDNA viruses; Parvoviridae; Parvovirus.
1 (bases 1 to 5081)
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Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Pred. No. 1.7e-09;
0; Mismatches 1; Indels 0
Length 2019;
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Score 58.4; DB 6;
Pred. No. 1.7e-09;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Parvovirus NS1 variant"
                                                                                                                                                                                                                                                                                        DNA
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1. 2019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nsl variants
1077260-A 16 21-FEB-2001;
                                                                                                                                                                                                                                                                          Sequence 16 from Patent EP1077260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAC39997.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nueesch, J. and Rommelaere, J.
Parvovirus nsl variants
Patent: EP 1077260-A 16 21-FP
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  97.3%;
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Local Similarity 98.3%;
hes 59; Conservative (
Query Match 97.3
Best Local Similarity 98.3
Matches 59; Conservative
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The messenger RNA of this virus (colinear with the strand listed) is spliced, but the exact splice sites are not known. The listed strand is complementary to the one which is included in the virion. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILEKAETSKLTNFSLPDTRTCRIFAFHGMNYVKVCHAICCVLNRQGGKRNTVLFHGPA
STGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAGNFGQQVNQFKAIC
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LGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conflict with the conceptual translation; coding sequence"
Astell, C.R., Thomson, M., Merchlinsky, M. and Ward, D.C.
The complete DNA sequence of minute virus of mice, an autonomous
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2332. .2361
                                                                                    Nucleic Acids Res. 11 (4), 999-1018 (1983)
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                                                                                                                   83143341
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Uniquinous bounce taken in minute vitue of manages to in mouse 1 (variant A.9) cantains two groups that infect mammalian hoses: (i) defective (helper-dependent) adeno-associated viruses, and (ii) autonomous (helper-dependent) adeno-associated viruses, and (ii) autonomous (helper-dependent) parvoviruses. MWM is a member of the latter group. Both groups have been demonstrated to package both plus and minus strands (in separate particles) of the ss-DNA genome, though the minus strand is more typically packaged in the latter group.

The sequence below corresponds to the plus (+) strand, also referred to as the C-strand. The minus (-) strand is also referred to as the V-strand.

The 3' the remaini both exhibit the potential for forming stable 'fold-back' hairpins; these sequences appear to play a role in replication [1].

The left and right halves of the genome encode two distinct, but overlapping transcriptional units. The transcripts can be summarized [1] (1 map.unit (mu) = 51 bp):

R1 (48 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu
R2 (3.3 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu
R3 (3.0 kb): 40 mu - 46 mu; 46+ mu - 95 mu
R3 (3.0 kb): 40 mu - 46 mu; 46+ mu - 95 mu
R3 is the major transcript.

There are two major open reading frames, both on the plus (or C) strand. The left side ORF probably encodes a non-capsid protein of 85 kd; the right side ORF probably encodes the viral
                                                                                                                                                                                                                                                                                                                               1400
SVRYSYGKQHGENWASHGPAPERYTWDETSFGSGRDTKDGFIQSAPLVVPPPLNGILT
NANPIGTKONDIHSSNVFNSYOSPLTABEHSPVYPOPQQYWDKELDLEHKRRLHTTAPFV
CKNNAPGQMLVRLGPNLTDQYDPNGATLSRLYTYGTFFWKGKLTMRAKLRANTTWNPV
YQVSAEDNGNSYMSVTKWLPTATGNMQSVPLITRPVARNTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRL 22-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Original source text: Minute virus of mice (strain MVM(p)), passed
                                                                                                                                                                                                                                                                             09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Astell, C.R., Gardiner, B.M. and Tattersall, P. DNA sequence of the lymphotropic variant of minute virus of mice, MVM(1), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Astell, C.R., Thomson, M., Merchlinsky, M. and Ward, D.C.
The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                        Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (bases 1 to 5149)
                                                                                                                                                                                                                                                                          1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                        ..
0
                                                                                                                                                                      Length 5081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minute virus of mice, complete genome.
JO2275 M12520 M12521 M14704
JO2275.1 GI:3322923
JO2775.1 GI:332293; capsid protein; complete genome;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                              Score 58.4; DB 14;
Pred. No. 1.7e-09;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5149 bp ss-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morgan, W.R. and Ward, D.C.
Three splicing patterns are used to
to all minute virus of mice RNAs
J. Virol. 60 (3), 1170-1174 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prototype strain
J. Virol. 57 (2), 656-669 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nonstructural protein.
Mice minute virus
Mice minute virus
                                                                                                                                                                97.3%;
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                                                                                                                                                                      Query Match
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/translation="Mappakrakrgwvppgykylgpgnslddgeptwpsdaaakehde
Aydoyiksgrupylyfsaadorfidotkdakowggkyghyfpfrtkaarapklatdsep
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Rvbraadgpgcsgggsggggygrgrstsydnythyrplagwybithaatrlyhlnnw
Ksenycrirvhnytdssykgnmakddaareqiwtpwslvdanawgvwlopsdwqyicut
                                                                                                                                                                                                                                                                                                                                                                                                    MSQLNLVSLDQEI FNVVLKTVTEQDLGGGÄIKIYNNDLTACMMVAVDSNNILFYTPAA
MSMETLGFY WKFUT IASPYKYTKCVDNEDSVTYENDGGTVEHVWGFYENSKONSOFFTI
NSMQDITLIRTGDERATGTYY POTNSVKLTHFWQTNRQLGOPPLLSTFPRADDAGTI
TAQGSRHGTTQMGVNWVSEAIRTRPAQVGFCQPHNDFBASRAGPPAAPKVPADITQGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKEANGSVRYSYGKOHGENWASHGPAPERYTWDETSFGSGRDTKDGFIQSAPLVVPPP
INGILINDANPETGYRDIHFSNVFNSGELTAREHSPYYDGOGWMKEEDLEHKRRLH
ITAFFVCKNAAPGOLVRLGENLTDOYDPNGATLSRIVTYGTFFWKGKLTWRAKLRAN
TTWNPVYQVSAEDNGNSYMSVTKWLPTATGNMOSVPLITRPVARNTY"
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QVGFCQPHNDFEASRAGPFAAPKVPADITQGVDKEANGSVRYSYGKQHGENWASHGPA
PERYTWDETSFGSGRDTKDGFIQSAPLVVPPPLNGILTNANPIGTKNDIHFSNVFNSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="unknown protein"
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                                                         fnote="alternative intron"
join(2286. .2316,2399. .4557)
gene="VP1" .2316,2399. .4557)
gene="VP1"
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2354. .2398
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/db_xref="GI:825484"
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/gene="VP"
/note="VP intron (alt.)"
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/note="ORF1; putative"
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/note="ORF3; putative"
/codon_start=1
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/codon_start=1
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/db_xref="GI:332296'
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/gene="VP1"
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/gene="VP1"
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SQQTFWAGNAYSDEVLGATWMLKEKSNQEVFSFYEKNENVQLNGKDIGWBYKKELQE
DELKSLQRGAETTWDQSEDMEWETTVDBWTKKQVFIFDSLVKKCLFEVLANTKNIFPGD
VNWFVQHEWGKDQGAMTCHVLIGGKDFSQAQSKWMRRQLAVYWSRWLYTACNVQLTPAE
RIKLREIAEDNEWYTLLTYKHKQTKKDYTKCVLFGNMIAYYFLTKKKISTSPPRDGGY
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MAIAILHTHTLAGDRGLVPKNEWPHIONAUVROYGSTPASYCAKWGKVPDMSENWAE
PKVPTPINLLGSARS PFTTPKSTPLSQVYALTPLASDLEDLALEPWSTPNTPVAGTAE
TQNTCEPAGSRACQDGQLSPTWSEIEEDLRACEGAEPLKKDFSEPLNLD*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STGKSI I AQA I AQAVGNYGCYNAANYNPPFNDCTNKNL I WVEEAGNFGQOVNQFKA I C
SGQTIR I DQKGKGSKQ I EPTPV I MTTNENI TVVR I GCEERPEHTQPIRDRMLNI HLTH
TLPGDFGLVDKNEWPMI CAMLVKNGYQSTWAS Y CAKWGKVPDWSENWAEPKVPTPI NL
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YXKKELQBEBELKSLQRGAETTWDQSEDNEWETTVDEWTKKQVPIFDSLVKKCLEBVL
NTKNIFPGDVNWFVQHEWGROGWHCTVLJGGKDFSQAQGKWWRRQLNVYWSRWLVTA
CNVQLTPABERIKLERAEDNEWYTLLTYKHKQTYKKDYTKKVLFGNMIAYYFFKKTS
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ARTKTAFDLILEKAETSKLTNFSLPDTRTCRIPAFHGMNYVKVCHAICCVLNRQGGKR
NTVLFHGPASTGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAGNFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLSSDSGWKTNPLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRIQTKKEVSIK
TTLKELVHKRVTSPEDWMMQPDSYIEMAAQPGGENLLKNTLEICTLTLARTKTAFDL
capsid proteins, VP1 (or A, 83 kd), VP2 (or B, 64 kd), and VP3 (or C, 61 kd). But because of uncertainties about the precise splice points in the transcripts, the exact starts, stops and (possible) intron boundaries are not known.

revision 4804 4870 a-65bp-a in [2]; aa in [1] [2]

revises [1].

Location/Qualifiers
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KACQDGQLSPTWSEIBEDLRACFGAEPLKKDFSBPLNLD "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRI
                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10794"
/lab_host="mouse 1 (variant A-9) cell"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="nonstructural protein"
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                                                                                                                                                                                                                     1. .5149
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/strain="MVM(p)"
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/gene="VP"
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/gene="VP"
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/gene="VP"
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/gene="VP"
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/gene="VP"
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NTVLFHGPASTGKSI IAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEBAGNFGQ
QVNQFKAICSGQTIRIDQKGKGSKQIEPTVIMTTNENITVVRIGCEERPEHTQPIRD
                                                                        RMINIHLTHTLPGDFGLYDKNEWPMICAWLVKNGYQSTWASYCAKWGKVPDWSENWAE
PKVPTPINSLGSARSPFTTPKSTPLSQNYAITPLASDLEDLALEPWSTPNTPVAGTAE
TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKRDFSEPLNLD"
       ARTKTAFDLILEKAETSKLTNFSLPDTRTCKIFAFHGWNYVKVCHAICCVLNRQGGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTSGVSRAGKRTRPPAYIFINQARAKKKLTSSAAQOSSQTMSDGTSQPDGGNAVHSAA
RVBRAADGPGGSGGGGGGGGGVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMP
KSENYCRIRVHNTTDTSVKGNMAKDDAHEQIWTPWSLVDANAMGVWLQPSDWQYICNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSQLNLVSLDQEI FNVVLKTVTEQDSGGQÄI KI YNNDLTACMMVAVDŠNNI LPYTPAA
NSMETLGFY PWKPT I AS PYRYYFCVDRDLS VTYENQEGT I EHNVMGTPKGMNSQFFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNGILTNANPIGTKNDIHFSNVFNSYGPLTAFSHPSPVYPQGQIWDKELDLEHKPRLH
ITAPFVCKNNAPGQMLVRLGPNLTDQYDPNGATLSRIVTYGTFFWKGKLTMRAKLRAN
TTWNPVYQVSVEDNGNSYMSVTKWLPTATGNMQSVPLITRPVARNTY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MAPPAKRAKRGWVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENTOQITLLRTGDEFATGTYYFDTNPVKLTHTWQTNRQLGQPPLLSTFPEADTDAGTL
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                                                                                                                                                                                                                                                                                                                                           'note="minor transcription start site"
number=1
2010. .2281
                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="minor transcription start site"
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|gene="VP1"
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gene="VP1"
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protein_id="AAA69568.1"
'db_xref="GI:825478"
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'protein id="AAA69570.1"
'db_xref="G1:825479"
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/gene="VP1"
/note="alternative intron"
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|protein_id="AAA69569.1"
|db_xref="G1:332290"
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/codon_start=1
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/gene="VP"
2003. .2281
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/gene="VP"
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/gene="VP"
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/gene="VP1"
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/gene="VP1"
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/gene="VP1"
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                                                                                                                                                                                                                                            MVMICG 5085 bp 88-DNA linear VRL 05-JUL-1995 Minute virus of mice (MVM(i)), a lymphotropic variant of MVM, complete genome.
                           ö
                                                                                                    1341 ACAAGAACCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Original source text: Minute virus of mice (lymphotropic variant of MVM) DNA, clone pEG2222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="MISGSESLDQGAKRKWAWFKVYKQMLKSVTYPFFHSVSRDAQKE
SNQLTWAGNAYSDEVIGTTNWLKEKSNQEVFSFVFKTEDVQLNGKDIGWNNYKKELQE
DELKSLQRGAETTWDQSEDMEWESTVDEWTKKQVFIYDSLVKKCLFEVLSTKNIAPAD
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STGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAGNFGQQVNQFKAIC
SGQTIRIDQKGKGSKQIEPTPVIMTINENITVVRIGCEERPEHTQPIRDRMLNIHLTH
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LGSARSPFTTPKSTPLSQNYAITPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
KACQDGQLSPTWSEIEEDLRACFGAEPLKRDFSEPLNLD"
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TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVFTTAQETKRGRI
OTKKEVSIKTTLKELVHKRVTSPEDMMMQPDSYIEMMAQPGGENLLKNTLEICTLTL
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FLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAOETKRGRIOTKKEVSIK
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nnykkeloedbelkslorgaettwdosedmewestvdemtkkovfiydslvkkclffvl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Astell, C.R., Gardiner, E.M. and Tattersall, P. DNA sequence of the lymphotropic variant of minute virus of mice, MVM(1), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (bases 1 to 5085)
                                                                        1 ACAAGAGCCTGCAGAATTTTTGCTTGCCTGGAACTATGTTAAAGTTTGCCATGCT
                           Gaps
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                         1; Indels
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protein_id="AAA69566.1"
db_xref="G1:825477"
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| Mol_type="genomic DNA"
| isolate="lymphotropic variant"
| db_xref="taxon:10794"
Pred. No. 1.7e-09;
0; Mismatches 1
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/product="nonstructural_p
/protein_id="AAA69567.1"
/db_xref="GI:332291"
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1. .5085
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                                                                                                                                                                                                                                                                                                                                                                  alternative splicing; on nonstructural protein.
  98.3%;
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/gene="NS1"
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/gene="NS1"
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Best Local Similarity 98.3
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Mice minute virus
Mice minute virus
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86115415
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TITLE
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MEDLINE
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Query Match
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                                                                                                                                                                                                         /codon_start=1
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GGQAIKIYNNDLTACOMMYAUDSNNILPYTPAANSMETLGFYPWKPTTASPYRYFCVD
RDLSVTYENQEGTIEHNVMGTPKGMNSQFFTIENTQQITLLRTGDEFATGTYYFDTNP
VKLTHTWQTNRQLGQPPLLSTFPPADTDAGTTTAGGSRHGATQWNSWANSTRTRPA
QVGFCQPHNDFESARAGPFAAPKVPADVTQGTDRANGSYRGYGKGHGSNWAAHGPA
PERYTWDETNRGSGRDTRGFIQSAPLVVPPPLNGILTNAANPGGMLVMLSRTRPA
QCGCQPHNDFESARAGPFAAPKVADTAGTGTTAGATTTANANPGGMLVMSY
RDLTARFSHPSPVYPQGQIMDKELDLEHKPRLHITAPFVCKNNAPGGMLVRCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; seDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

1 (bases 1 to 5087)
Sahli,R., McMaster,G.K. and Hirt,B.
DNA sequence comparison between two tissue-specific variants of the autonomous parvovirus, minute virus of mice
Nucleic Acids Res. 13 (10), 3617-3633 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAMVMI 5087 bp DNA linear VRL 01-JUL-1999 parvovirus minute virus immunosuppressive variant genome ( =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For the fibroblast-specific strain (MVMp) sequence see <PAMVM2>. The genomes of MVMp and MVMi (immunosuppressive variant) have more than 96% of their sequence in common.

Data kindly reviewed (18-JUL-1986) by G. McMaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coat protein; genome; origin of replication; overlapping genes; terminal repeat; unidentified reading frame. Mice minute virus Mice minute virus
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 92.0%; Score 55.2; DB 14; Length 5085; 1 Similarity 95.0%; Pred. No. 2.1e-08; 57; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .5087
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1. .116
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                                     'translation="MFNYLFYRPEITWF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="coat protein"
protein_id="AAA69571.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1085 bp updstream of EcoRI site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FATGNMQSVPLITRPVARNTY"
                      db xref="GI:825480"
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/note="TATA box"
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                                                                                                                         2795. .4558
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2795. .4558
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                                                             2400. .>4558
/gene="VP1"
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                                                                                                          'number=2
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PAMVMI
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VERSION
KEYWORDS
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TITLE
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PUBMED
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                                                                                                                                                                      CDS
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GGGGGGGGGVGYGSTGSYDDOTHYFFLGDGWVTIALATRUNILNMPKSENYCRIRVH
TTDTSYKGSNAARDDAHEGI WTPWSLVDANAWGWALQPSDWQYI CNTWSQLNIVYSLDG
I FNVVL.KTVTEQDSGGQAI KI YNNDLTACMMANDSNNI LEYTDAANSMETLGFYPWK
DEPATGFYYYPTONDLGYYTENDGGTI EHWWGTPKGMNSOFFI ENTQOITLLRTG
DEFATGTYYFDTNWYKLTHYMOTNRQLGOPPLLSTFPBADTDAGTLTAGGSRHGATQN
EVNWYSEAI RTRRAQUGFCQPHNDFEASRAGPFAAPKVPADNTQGVDREANGSVRYSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKQHGENWAAHGPAERYTWDETNFGSGRYDDGFIQSAPLVVPPPLAGILTANPIQ
TKNDIHFSNVFNSYQPLTAFGHPSPYYPQGQTWDKELDLEHKRRLHTAFPVCKNNPIG
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QYDPNGATLSRIVTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKWL
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Besselsen, D. G., Pintel, D. J., Purdy, G. A., Besch-Williford, C. L., Franklin, C. L., Hook, R. R. Jr. and Riley, L. K.

Molecular characterization of newly recognized rodent parvoviruses 96201434
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/note="polyadenylation signal"
4821. .4826
/note="polyadenylation signal"
4878. .5087
/note="terminal hairpin region"
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/gene="VP2"
<2792. .4558
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FEATURES

ORIGIN

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1202 ACAAGAACCTGCAAGATCTTTGCTTTTCATGGCTGGAACTACATTAAAGTTTGCCATGCT 1261
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Mouse parvovirus 1c
Viruses; sabNA viruses; Parvoviridae; Parvoviruses; sabNA viruses; Parvoviridae; Parvoviruses; Parvoviruses; 1 (bases 1 to 464)
Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses
J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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                 Viruses, ssDNA viruses, Parvoviridae, Parvovirinae, Parvovirus.

1 (bases 1 to 4764)

Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.

Molecular characterization of newly recognized rodent parvoviruses
J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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                                                                                                                                                                                                                       Discrett Submission
Submitted (17-AUG-1995) David G. Besselsen, Department
Veterinary Pathology, University of Missouri-Columbia,
Veterinary Medicine Building, Columbia, MO 65211, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

84.0%; Score 50.4; DB 14; Length 4764;
Best Local Similarity 90.0%; Pred. No. 9.3e-07;
Matches 54; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (17-AUG-1995) David G. Besselsen, Department of Veterinary Pathology, University of Missouri-Columbia, Veterinary Medicine Building, Columbia, MO 65211, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
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|mol type="genomic DNR"
|specific host="Mus musculus"
|db_xref="teaxon:42842"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50.4; DB 14
Pred. No. 9.3e-07;
                                                                                                                                                                                                                                                                                                                                                          /organism="Mouse parvovirus 1b"
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/specific host="Mus musculus"
/db xref="taxon:42841"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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U34254
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1 Similarity 90.0%;
54; Conservative
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Besselsen, D.G.
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    Mouse parvovirus 1b
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Best Local S:
Matches 54
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ACCESSION
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KEYWORDS
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AUTHORS
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PUBMED
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae.
1 (bases I to 4761)
Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses
J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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                                                          Direct Submission
Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pethology, University of Missouri-Columbia, W213
Veterinary Medicine Building, Columbia, MO 65211, USA
Location/Qualifiers
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Submitted (17-AUG-1995) David G. Besselsen, Department
Veterinary Pathology, University of Missouri-Columbia,
Veterinary Medicine Building, Columbia, MO 65211, USA
                                                                                                                                                                                                                                                                                                                 Length 4773;
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Pred. No. 2.6e-07;
0; Mismatches 5; Indels
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                                                                                                                                                                                  /organism="Hamster parvovirus"
/mol_type="genomic DNA"
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/db_xref="taxon:42843"
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/strain="Cutter"
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nilarity 91.7%; 1
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Mice minute virus DNA.
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Besselsen, D.G.
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Besselsen, D.G.
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RESULT

Mouse parvovirus 1b

U34253.1

VRL 21-AUG-1996

linear

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Length 4764; Indels

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TSPRRDGGYFLSSDGWKTNFLKEGERHLUSKLYTKCVLFGNMIAYFLTKKKIS
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JOINIC 2290. 2320, 2403. .4561)
/gene="VPI"
                    MPU12469
S144 bp DNA linear VRL 24-JAN-1995
Mouse parvovirus 1 complete genome, nonstructural protein 1 (NS1)
gene, complete cds and capsid protein (VP1) gene, complete cds.
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TRGDRSGITQISGSNDVTEATRVRPAQVGFCQPHDNFETSRAGPFKVPVVPANVTQGN
EHDANGSLRYTYDKQHGQDWGSNNSKERFTWDAISYDSGRWADRCFTINATPFTSPPAL
NILTINSDPIGNKTAIHYQVVFNSYGDLTAFPHPAPIYPQGQIMDKELDLEHKPRLHA
QAPFVCKNNAPGQLIVRLAPHNITDQYDPNSSTLSRIVTYGTFFWKGKLTLKAKLRPNA
TWNPVYQVSAQYQNENEYMSIHKWLPTATGNMQSIPLLSRPVARNTY"
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SKBNYCRWYRNTNDTRTAGNAAXDDAHEQIWFWBSLIDSNAMGWWFGSEDWQFTCNN
MSHYNLHSLDQELFWVVIKYVIKYTGARAKIYINNDLTASMWVALDSNNILPYTPAT
DNQETLGFYPWKPTMPSPYRYYFNCDRSLSVTYTDQTGSIVDTWANASGLSSQFFTIE
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STKNIAPADVTWFVQHEWGKDQGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRWLVTA
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GTSGVSIAGKRTKPPAHIFINQARAKKKRASLAAQQRTQTMSDGAEQPDSGSAVQSAA
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Mouse parvovirus 1
Mouse parvovirus 1
Viruses; saDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (bases 1 to 5144)
Ball-Goodrich, L.J. and Johnson, E.
Molecular characterization of a newly recognized mouse parvovirus J. Virol. 68 (10), 6476-6486 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ball-Goodrich, L. John Ball-Goodrich, E. Submission Submitted (20-UUL-1994) Lisa J. Ball-Goodrich, Section of Comparative Medicine, Yale University School of Medicine, New Haven, CT 06520-8016, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .5144
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/product="nonst
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Score 50.4; DB 14; Length 5144; Pred. No. 9.3e-07;

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Query Match Best Local Similarity

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Search completed: June 2, 2004, 18:58:36 Job time : 653 secs

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Aad02799 Parvoviru
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Aar18321 Attenuate
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Aab1601 Human GPC
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Aa809301 Human sch
Aad44606 Ohicken D
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Aak68375 Human Imm
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ABZ35015 AAK98324 AAK10099 AAK10099 ADB57189 ABZ16033 AAK15544 ABV51185 ABV5218 AAK294174 AAK29491 AAK29491 AAK29489 ABX17941 AAK17940 AAK17940	ALIGNMENTS	ВР.			protein 1 (N	ein 1; cytostatic therapy; mutant;		ifiers irvovirus loes not				نہ	KREBSFORSCHUNGSZENTRUM.			ure protei Eted equil nd cytotox
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222 222 222 222 222 222 222 222 222 22		02800	AAD02800;	-AUG-2003	Parvovirus	NS1; non-structure prot tumoural disease; gene	Parvovirus Synthetic.	CDS CDS mutation	EP1077260	-FEB-200	-AUG-199	-AUG-199	(DEKR-) DEUT	Nueesch J,	WPI; 2001-2127 P-PSDB; AAY727	Novel parvovirus non-stru tumoral diseases, has a s transcription activities,
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0 000 00 0 '0000000		RESULT 1 AAD02800	<b>4</b> 2	<b>1</b> 111	X E S	\$ <u>\$</u> <b>\$</b> \$	S S S	X	XX	X C	X & ;	¥ # ;	<b>48</b> 5	\$ II \$	\$ # # \$	A T T T

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Gaps

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0; Indels

100.0%; Score 60; DB 5; L 100.0%; Pred. No. 1.2e-11; ive 0; Mismatches 0;

Query Match Best Local Similarity 100. Matches 60; Conservative

8

Length 2019;

Sequence 2019 BP; 697 A; 389 C; 453 G; 480 T; 0 U; 0 Other;

therapy. (Updated on 06-AUG-2003 to correct OS field.)

SXS

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1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT

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                                                                              The present sequence is a parvovirus non-structure protein 1 (NS1) variant (T363A) DNA fragment. The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytocoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-NUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; muteln; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/product= "NS1 variant (T363A) protein"
replace(1187, A)
/*tag= b
                                                                                                                                                                                                                                                                                                                   Sequence 60 BP; 15 A; 11 C; 13 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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1. .2019
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                           Disclosure; Page 16; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD02801 standard; DNA; 2019 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99EP-00115161
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                                                                                                                                                                                                                                                                                                                                                                                                                                      60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1999;
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31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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AAD 02801
ID AAD
XXX AAD 02801
DT 31-
XXX NS1
X & X & O O O O O O O X & S
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1081 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a DNA encoding parvovirus non-structure protein (NS1) variant (T463A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytocoxidity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vociors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
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                                                                                                                                                                                     Parvovirus non-structure protein 1 (NS1) variant (T463A) DNA.
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                                                                                                                                                                                                                                                                                                                                                "NS1 variant (T463A) protein"
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .2019
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                                                                                                                                                                                                                                                                                                                              /*tag= a /product= "NS1 va.
replace(1387, A) /*tag= b
                                                                               AAD02805 standard; DNA; 2019 BP
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                                                                                                                                          (revised)
(first entry)
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31-MAY-2001
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                                                                                                                                                                                                                                                           Parvovirus
                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                             AAD02805;
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Best Local (
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                                                   RESULT 3
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1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGCTGGAACTATGTTAAAGTTTGCCATGCT 60

The present sequence is a DNA encoding parvovirus non-structure protein (NS1) variant (T363A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cyclocoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene

Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.

WPI; 2001-212717/22.

P-PSDB; AAY72706.

Claim 7; Page 16-19; 41pp; English.

2019
/\*tag= a
/product= "Parvovirus NS1 protein"

99EP-00115161. 99EP-00115161

Location/Qualifiers

(revised)
(first entry)

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NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                        Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                               Parvovirus non-structure protein 1 (NS1) wild-type DNA
                                                                                                                                                                                                                                                                                         (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 41pp; English
                                                                                                                                                                                                                                                                                                                Nueesch J, Rommelaere J;
                                                                                                                                                                                                                                                                                                                                   WPI; 2001-212717/22.
P-PSDB; AAY72702.
                                                                                                                                                                                                                                          13-AUG-1999;
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             06-AUG-2003
31-MAY-2001
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                                                                                                          Parvovirus
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1081 ACAAGAACCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a DNA encoding parvovirus non-structure protein (NS1) variant (T394A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                               NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58.4; DB 5; Length 2019;
Pred. No. 4.4e-11;
0; Mismatches 1; Indels 0
                                                                                                                                                         Parvovirus non-structure protein 1 (NS1) variant (T394A) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2019 BP; 697 A; 389 C; 453 G; 480 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                            /*tag= a
/product= "NSI variant (T394A) protein"
replace(1180, A)
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                    KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 22-24; 41pp; English
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                                                                       AAD02803 standard; DNA; 2019
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                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                .2019
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es 59; Conservative
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                                                                                                                    06-AUG-2003
31-MAY-2001
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                                                                                                                                                                                                                   Parvovirus
                                                                                                                                                                                                                               Synthetic
                                                                                               AAD02803;
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Best Local S
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1140
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The present sequence is a wild type DNA encoding parvovirus non-
structure protein 1 (NS1). The present invention relates to the variants
of the parvovirus non-structure protein (NS1) having a shifted
equilibrium between the DNA replication and transcription activities, and
the cytotoxicity activity. These variants are useful as toxins for
treating tumoural diseases. The variant DNAs are useful as vectors for
gene therapy. (Updated on 06-NUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                         1081 ACAAGAACCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                                                              1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                                                                                                                                                                              Query Match 97.3%; Score 58.4; DB 5; Length 2019; Best Local Similarity 98.3%; Pred. No. 4.4e-11; Matches 59; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parvovirus non-structure protein 1 (NS1) variant (S283A) DNA
                                                                                                                                                                                                    Sequence 2019 BP; 698 A; 389 C; 452 G; 480 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD02799 standard; DNA; 2019 BP
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31-MAY-2001
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Synthetic.
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1081 ACAAGAACCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 1140

AAD02797 standard; DNA; 2019 BP

RESULT 5
AAD02797
ID AAD0
XX
AC AAD0

AAD02797

1 ACAAGAGCCTGCAGAATTTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 60

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1084 ACAAGAACATGTAAAATATTCAGCATGCACAATTGGAACTACATTAAAGTCTGCCATGCT 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parvovirus; dog; vaccine; CPV; myocardial disease; enteric disease; ds;
                                                                                                                                                                                                                                              Polypeptide obtd. by recombinant DNA methods - for vaccination against parvovirus infections in man and animals.
                                                                                                                                                                                                                                                                                                                                 The inventors claim an immunologically active polypeptide for the development of vaccinal immunity against parvovirus infection. Also claimed are DNA sequences wholly or partly duplicative of defined sequences. The polypeptides are used in vaccines for conferring protection against parvovirus infections in man and animals. (Updated 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This viral DNA is isolated from a non- attenuated CPV. The DNA is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.0%; Score 31.2; DB 1; Length 3524; ilarity 70.0%; Pred. No. 0.32; Conservative 0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3524 BP; 1400 A; 719 C; 648 G; 757 T; 0 U; 0 Other;
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CPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Attenuated CPV strains contg. up to 4 mutation virus - useful as a veterinary vaccine against such as wild or domestic dogs.
                                                                                                                                                                                                                                                                                                   Claim 10; Table II, Page 33-49; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gruenberg A, Carmichael LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 21-24; 42pp; English.
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                                   84WO-US000063
                                                                    83US-00459203.
84US-00567968.
                                                                                                                                                                                                WPI; 1984-201354/32.
P-PSDB; AAP40306, AAP40675.
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es 42; Conserv
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                                                                                                                         (AMGE-) AMGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-1994;
                                   19-JAN-1984;
                                                                    19-JAN-1983;
06-JAN-1984;
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02-AUG-1984.
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                                                                                                                                                             Fox GM;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a DNA encoding parvovirus non-structure 1 protein (NS1) variant (S283A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                            Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACAAGAGCCTGCAGAATTTTTGCTTGCTGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence from the double-stranded replicative form DNA of porcine parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2019 BP; 698 A; 389 C; 453 G; 479 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein envelope; immunogen; vaccine; antigen; epitope; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                     "NS1 variant (S283A) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58.4; DB 5;
Pred. No. 4.4e-11;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porcine parvovirus; NADL-2 virulent strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/note= "see AAP40675"
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/note= "see AAP40306"
2107. .3522
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   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 11-14; 41pp; English
                                      /*tag= a /product= "NS1 v replace(847, A) /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAN40252 standard; DNA; 3524
                                                                                                                                                                                                   99EP-00115161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.3%;
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                                                                                                                                                                                                                                                                                                             Nueesch J, Rommelaere J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 98.3
es 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .2073
                        .2019
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Query Match

Matches

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24-OCT-2003 12-JAN-1992

AAN40252;

WO8402847-A.

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Gaps

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relative to control disease in animals,

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WPI; 2001-212717/22. P-PSDB; AAY72704.

13-AUG-1999; 13-AUG-1999;

EP1077260-A1

mutation

Key

21-FEB-2001

88888888

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Sequence 5049 BP; 1790 A; 814 C; 1029 G; 1416 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canine parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9742972-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-1997
                                                                                                                                                                                                                                                                                                                                              21-MAY-1998
                                                                                                                                                                                                                                                                                                       AAT88321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                               feline
                                                                                                                                                                                                                          RESULT 10
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                                                                                                                                                                                                                                                                                CTAGAACATGTCAAATTTTTAGAATGCACGGATGGAATTGGATTAAAGTTTGTCACGCT 1415
preferably derived from vB1440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pGEM3Z or pGEMSZ. The host cells to be transfected ar selected from Norden Laboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This viral DNA is isolated from an attenuated CPV. The DNA is preferably derived from vBI440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pGEM3Z or pGEM5Z. The host cells to be transfected ar selected from Norden Laboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells or canine A72 cells
                                                                                                                                                                                                                                             2 CAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parvovirus; dog; vaccine; CPV; myocardial disease; enteric disease; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Attenuated CPV strains contg. up to 4 mutation (s) relative to control virus - useful as a veterinary vaccine against CPV disease in animals, such as wild or domestic dogs.
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                        ö
                                                                                                                         Sequence 5049 BP; 1791 A; 812 C; 1029 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                               Length 5049;
                                                                                                                                                                                                      19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Attenuated canine parvovirus CPV-39 passage 60 DNA
                                                                                                                                                               Score 28.6; DB 2;
Pred. No. 3;
                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parrish CR, Gruenberg A, Carmichael LE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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'note= "A, G or T"
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note= "A, C
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/note= "A (
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                                                                                                                                                                                                        40; Conservative
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/note=
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                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canine parvovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-OCT-1996
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                                                                                                                                                                                                          Matches
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RESULT 9
AAT15312
AAT16
AAT16
AAT16
AAT16
AAT16
AAT16
AAT16
AAT17
AAT16

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                                                          1357 CTAGAACATGTCAAATTTTTAGAATGCACGGATGGAATTGGATTAAAGTTTGTCACGCT 1415
                                                                                                                                                                                                                                                                                                                             (G in passage
                                                                                                                                                                                                                                                                                                                                                                    равваде
                                                                                                                                                                                                                                                                                                                                                                                                          (A in passage
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nbase 4973 is C in virulent CPV-39 (T in passage
                     Gaps
                                      2 CAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                       parvovirus; CPV; attenuation; vaccine; dog;
panleukopenia virus; mink enteritis virus; infection; ds.
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                    ö
 Length 5049;
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/note= "base 4409 is C in virulent CPV-39
65_attenuated virus)"
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/note= "base 4477 is G in virulent CPV-39
65 attenuated virus)"
4889
                                                                                                                                                                                                                                                                                                                   /*tag= c
/note= "base 4307 is A in virulent CPV-39
65 attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
"base 4889 is C in virulent CPV-39
                                                                                                                                                                                                                                                                                                                                                                  in virulent CPV-39
                    Indels
                   19;
 DB 2;
                                                                                                                                                                                                                                                                    coding region"
                                                                                                                                                                                                                                                                                                 coding region'
                   0; Mismatches
 Score 28.6;
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gruenberg A;
                                                                                                                                                                   Attenuated canine parvovirus genomic DNA.
                                                                                                                                                                                                                                                                                                                                                /*tag= d
/note= "base 4350 is C in
65 attenuated virus)"
4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 attenuated virus) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 attenuated virus)"
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                           *tag= a
note= "NS1/NS2
                                                                                                           AAT88321 standard; DNA; 5049 BP
                                                                                                                                                                                                                                                                                               'note = "VP1/VP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US007584
Query Match
Best Local Similarity 67.8%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                            .4541
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                                                                                                                                                (first entry)
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us-10-069-056-7.rng

Thu Jun

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trenuated viruses are obtained by serial passage of the virulent.

type 2b isolate 39 in NLFK feline kidney host cells. They have one or more of the sequence alterations indicated in the sequence relative to the sequence of a control (5th passage) wild-type CPV-2b (see AAT88320).

A claimed virus from the 65th passage (deposited as ATCC VR 2528)

Contains all 6 mutations. The DNA from attenuated CPV strains (see also which, in turn, can be transfected into cells to generate master stocks which, in turn, can be transfected into cells to generate master stocks of the virus. The attenuated viruses can be used in dogs as a vaccine to protect against CPV disease, or more generally in cats and minks to protect against feline panleukopenia virus and mink enteritis virus. The vaccines protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), providing a long term immune response. (NB. this sequence was created by adaptation of the wild-type CPV-2b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1357 CTACAACATGTCAAATTTTTAGAATGCACGGATGGAATTGGATTAAAGTTTGTCACGCT 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 60
                                                                                 annenuated canine parvovirus (CPV) genome
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
for protection against parvovirus and feline pan-leukopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= d
note= "base 97 is C or T in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canine parvovirus, CPV, attenuation, vB1440, vaccine, dog,
feline panleukopenia virus, mink enteritis virus, infection, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                   Sequence 5049 BP; 1788 A; 809 C; 1029 G; 1417 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                             Score 28.6; DB 2; Length 5049;
Pred. No. 3;
0; Mismatches 19; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= f
/note= "base 4881 is C in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= e
note= "base 4745 is T in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/note= "base 59 is G in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Attenuated canine parvovirus (vBI440) genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag= a
note= "NS1/NS2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "VP1/VP2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canine parvovirus; vBI440 (ATCC VR 2489)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT88324 standard; DNA; 5049 BP
                                                Claim 1; Page; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                  67.8%;
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Matches 40; Conservative
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21-MAY-1998
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 vaccines
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passaging (60 times) of virulent canine parvoirus (CPV) type 2b isolate 39 in NLFK feline kidney host cells. The attenuated virus is designated velials (ATCC VR 2489). It contains 4 mutations relative to the sequence (see AAT88320) of the control (5th passage) wild-type CPV-2b. 2 Mutations are within the hairpin formed by the 3' terminal palindrome: the mutation at nucleotide 59 introduces an A into a G-C rich region within the tip of the hairpin, disrupting the base pairing in one of the 2 small internal palindromes within the palindromes within the palindrome. The DNA from attenuated CPV strains (see also AAT88321) is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks of the curson. The attenuated viruses can be used in dogs as a vaccine to protect against CPV disease, or more generally in cats and minks to protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), providing a long term immune response.

(Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                     Canine parvovirus DNA carrying specific attenuating mutation(8) - used as vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1357 CTAĞAACATGTCAAATTTTTAGAATGCACGGATGGAATTGGATTAAAGTTTGTCACGCT 1415
                                                                                                                                                                                                                                                                                   DNA sequence comprises an attenuated virus genome derived by serial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parvovirus; CPV; attenuation; vBI440; vaccine; dog;
panleukopenia virus; mink enteritis virus; infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5049 BP; 1791 A; 812 C; 1029 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.7%; Score 28.6; DB 2; Length 5049; 67.8%; Pred. No. 3; ive 0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273. .2279
/*tag= a
/note= "NS1/NS2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b
/note= "VP1/VP2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canine parvovirus 39 passage #5 (wild-type).
                                                                                                        Carmichael LE, Gruenberg A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canine parvovirus; type 2b isolate 39
                                                                                                                                                                                                                                                Example 8; Page 34-37; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT88320 standard; DNA; 5049 BP.
                                                                     (CORR ) CORNELL RES FOUND INC
97WO-US007584.
                                  96US-00647655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .4541
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 67.8
Les 40; Conservative
06-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9742972-A1.
                                  15-MAY-1996;
                                                                                                        Parrish CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2003
21-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT88320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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The present sequence represents the complete genome of Chlamydia trachomatis. Open reading frames (ORFs) of the genome encode polypeptides AAY36734-Y37949. The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, pepidymitis, cervicits, alpingitis, perihepatitis, barkholinitis, peneumopathy in breast feeding infants; and venereal lymphogramulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38590 AGAGCATGTAGATCTTTTACGAGTAGGGCCTCGCAATATGCAAAATTTTGTCTTGCT 38646
                                                                                                                                                                                                                                                                      Vaccine, eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genical disease; perthepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1038602 BP; 304265A; 214645C; 214259G; 305001T; 0U; 432Other;
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                                                                                                                                                                                                                                   Complete genome sequence of Chlamydia trachomatis.
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Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome sequence of Chlamydia trachomatis.
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                  710000
810000
910000
1010000
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AAZ01425 BEandard; DNA; 1038602 BP.
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97FR-00016034.
98US-0107077P.
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ilarity 66.7%;
Conservative (
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1000001
                  600001
700001
800001
                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                         Chlamydia trachomatis
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Les 38; Conserv
                  AAZ01425_06
AAZ01425_07
AAZ01425_08
AAZ01425_09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET
AAZ01425 05
                                                                                                                                                                                                                                                                                                                                                                                                             WO9928475-A2
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ID AAF9
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AC AAF9
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DT 23-M
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Continuation (4 of 4) of ADE11169 from base 300001 (Human transporter protein encoding
WP Sequence split into 4 fragments LOCUS ADE11169 Accession Ade11169
WP ADE11169_0 100000 110000
WP ADE11169_1 100000 100000
WP ADE11169_2 200001 310000
WP ADE11169_2 300001 394191
                                                                                                                                                                                                                                                                                                                                          This DNA sequence comprises the genome of virulent canine parvovirus type 2D (CPV-2b) isolate 39, obtained after 5 serial passages in NLFK feline kidney host calls. Purther passaging has yielded attenmated virus wB1440 (ATCC VR 2489) (see AAT88324) from the 60th passage, and a claimed virus C see AAT88321) derived from the 65th passage (ATCC 2528). These crespectively contain 4 and 6 mutations in comparison to the virulent 5th passage virus. The DNA from attenuated CPV-2b strains is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into calls to generate master stocks of the virus. The attenuated viruses can be used in dogs as a vaccine to protect against CPV disease, or more generally in cats and minks to protect against felline panleukopenia virus and mink enteritis virus. The vaccines protect against felline panleukopenia virus and mink enteritis virus. The vaccines protect gainst cypes 2 and 2a), and provide a long term immune response. (Updated on 17-0CT-2003 to standardise OS field)
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                                                                                                                                                                                                                               Canine parvovirus DNA carrying specific attenuating mutation(s) - used as vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5049;
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Pred. No. 25;
0; Mismatches
                                                                                                                                                       Gruenberg A;
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Fragment Name Begin
ADE11169 100001
ADE11169 2 200001
ADE11169 3 300001
                                                                                                            (CORR ) CORNELL RES FOUND INC
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                                    97WO-US007584
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                                                                                                                                                       Parrish CR, Carmichael LE,
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Matches 40; Conservative
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P Sequence split into 11 E1
P AAZO1425 00
P AAZO1425 02 21
P AAZO1425 03 33
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                                      06-MAY-1997;
                                                                          15-MAY-1996;
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Best Loc Matches

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AAZ01425\_
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Ouery Match 42.7%; Score 25.6; DB 4; Length 396; Best Local Similarity 63.8%; Pred. No. 21; Matches 37; Conservative 0; Mismatches 21; Indels (

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Gaps

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Search completed: June 2, 2004, 19:08:30 Job time: 149.25 secs

App Appl 5, Ap Appl

Sequence

1283, Ap 7, Appli 1284, Ap 463, App 29, Appl 5, Appli

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Sequence Sequence

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Run on:

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2 CAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 60
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Pred. No. 0.37;
0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Parrish, Colin R.
APPLICANT: Gruenberg, Allen
APPLICANT: Carmichael, Leland E.
ATTLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/336,345
                                                                                                                                              US-09-606-421B-151
US-09-221-107-151
US-08-30-691B-21
US-08-30-651-1315
PCT-US93-655-1335
US-08-961-527-210
US-08-961-527-210
                         US-09-134-000C-1283
US-09-287-599A-7
                                                                                          US-08-365-981-5
US-09-643-597-151
US-09-480-884A-151
US-09-542-615A-151
                                                  US-09-107-532A-1284
US-09-107-532A-463
US-09-277-565-29
                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30753
REFERENCE/DOCKET NUMBER: 7937-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER.STICS:
LENGTH: 5049 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSEE: Pennie & Edmonds
T: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08336345 Patent No. 5814510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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                         1038
1128
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Best Local Similarity
Matches 40; Conserv
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2
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ORGANISM: Par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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CITY: Ne
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3, Appli
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Sequence 156, App
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Sequence 2, Appli
Sequence 1, Appli
                                                                                          2, 2004, 18:58:44 ; Search time 32.75 Seconds (without alignments) 1016.704 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 938,
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Sequence
Sequence
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Sequence
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                                                                                                                                                                             1 acaagagcctgcagaatttt......atgttaaagtttgccatgct
                                                                                                                                                                                                                                                                                                                                                                                               Issued Patents NA:*

'GqnZ 6/ptodata/2/ina/5A COMB.seq:*
'GqnZ 6/ptodata/2/ina/5B COMB.seq:*
'GqnZ 6/ptodata/2/ina/6A COMB.seq:*
'GqnZ 6/ptodata/2/ina/6B COMB.seq:*
'GqnZ 6/ptodata/2/ina/PCTUS COMB.seq:*
'CqnZ 6/ptodata/2/ina/PCTUS COMB.seq:*
'GqnZ 6/ptodata/2/ina/backfllesl.seq:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-336-345-2
US-08-647-655-1
US-09-640-173-156
US-09-640-173-156
US-09-713-550-156
US-09-713-550-156
US-09-328-332-3500
US-09-345-468-15
US-09-414-453A-15
US-09-414-453A-15
US-09-345-468-12
US-09-346-468-14
US-09-340-236-901
US-09-56-902-28
US-09-56-002-28
US-09-596-002-28
US-09-846-2698-3
US-08-486-2698-3
US-08-486-2698-3
US-08-486-2698-3
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-09-621-976-9809
                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                              682709 segs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   nucleic search, using sw model
                                                                                                                                                                                                                   Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                     seq length: 0
seq length: 2000000000
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Match Length DB
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42.7 319608
39.7 861
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509
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1357 CTAGAACATGTCAAATTTTTAGAATGCACGGATGGAATTGGATTAAAGTTTGTCACGCT 1415
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US-08-647-655-1
| Sequence 1, Application US/08647655
| Patent No. 588586|
| GENERAL INPORMATION:
| APPLICANT: Gruenberg, Allen
| APPLICANT: Gramichel, Leland E.
| TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
| MUMBER OF SEQUENCES: 2
| CORRESPONDENCES: 2
| ADDRESSEE: Pennie & Edmonds
| STREET: 1155 Avenue of the Americas
| CITY: New York
| STATE: New York
                                                                                                                                                Sequence 2, Application US/08336345

Patent No. 5814510

GENERAL INFORMATION:
APPLICANT: Parrish, Colin R.
APPLICANT: Gruenberg, Allen
APPLICANT: Gruenchael, Leland B.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: New York
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 47.7%; Score 28.6; DB 1; Length 5049; Best Local Similarity 67.8%; Pred. No. 0.37; Matches 40; Conservative 0; Mismatches 19; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITI: New YORK

ZIP: 10036-2711

COMPUTER READBALE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,345
FILING DATE:
CLASSIFICATION NUMBER: US/08/336,345
ATTONEY AGORDA, Jannifer
REGISTRATION NUMBER: 30753
REFERENCE/DOCKET NUMBER: 30753
REFERENCE/DOCKET NUMBER: 7937-006
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 790-9090
TELEPAX: (212) 790-9090
TELEPAX: (212) 780-100
TELEPAX: (212) 790-9090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Parvovirus
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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MOLECULE TYPE: DN
HYPOTHETICAL: NO
                                                                                                                              US-08-336-345-2
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21P: 10036-2711.

CONDUTER READALE FORM:
WEDITATY TEST: 10094 disk

CONDUTER: 1287 COMPANIES.

SOFTWARE STATES.

CONDUTER: 1287 COMPANIES.

SOFTWARE STATES.

CONDUTER: 1287 COMPANIES.

SOFTWARE STATES.

APPLICATION NUMBER: 105763.

FREEDRING: 1210 195-09647 655

FREEDRING: 1210
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                                                                                                                                                                                                                                                                                                                                                                            2 CAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
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US-09-713-550-156
US-09-713-550-156

Sequence 156, Application US/09713550

Patent No. 6617109

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C4

CURRENT APPLICATION NUMBER: US/09/713,550

CURRENT APPLICATION NUMBER: US/09/713,550

CURRENT APPLICATION OF 2000-11-14

NUMBER OF SEQ ID NOS: 205

NUMBER OF SEQ ID NOS: 205

SOFTWARE: FRASESO for Windows Version 3.0
                                                                                                                                                                                                                                                                           Length 5049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 42.7%; Score 25.6; DB 4; Length 396; Best Local Similarity 63.8%; Pred. No. 2.6; Matches 37; Conservative 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                         19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 210121.484C2
CURRENT APPLICATION NUMBER: US/09/640,173
CURRENT FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 196
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                      Query Match
47.7%; Score 28.6; DB 2;
Best Local Similarity 67.8%; Pred. No. 0.37;
Matches 40; Conservative 0; Mismatches 19;
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Patent No. 6613515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | NAME/KEY: misc_feature
| LOCATION: (1)...(396)
| OTHER INFORMATION: n = A,T,C or G
US-09-640-173-156
                                                                                                MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
LENGTH: 5049 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                              ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
                                                                            unknown
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-640-173-156
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LENGTH: 396
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## PAPLICANT: BAIDAIN, DELIGAL,
## PAPLICANT: BAIDAIN, DELIGANT:
## PAPLICANT: BAIDAIN, BERIOUX, LAURENT
## TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
## FILE REFRENCES: GENEST: 0.4702
## CURRENT PAPLICATION NUMBER: US 60/126,903
## PRIOR PAPLICATION NUMBER: US 60/126,903
## PRIOR FILING DATE: 1999-03-30
## PRIOR FILING DATE: 1999-04-30
## PRIOR FILING DATE: 1999-04-30
## PRIOR FILING DATE: 1999-04-30
## PRIOR FILING DATE: 1999-07-27
## PRIOR FILING DATE: 1999-07-29
## PRIOR FILING D
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                                                                                                                                                                                                                                                                                                                                                                                                                             3 AAGAGCCTGCAGAATTTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 60
                                                                                                                                                                               Query Match
42.7%; Score 25.6; DB 4; Length 396;
Best Local Similarity 63.8%; Pred. No. 2.6;
Matches 37; Conservative 0; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 18778..18862
OTHER INFORMATION: exon Bbis g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
LOCATION: 25593..25740
OTHER INFORMATION: exon C 935018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: exon A 935018 gene FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09539333D Patent No. 6476208
i LOCATION: (1)...(396)
i OTHER INFORMATION: n = A,T,C or G
US-09-713-550-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Bougueleret, Lydie
APPLICANT: Bihain, Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc feature
LOCATION: 31..1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 14877..14920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1108..1289
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LOCATION: 1108
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us-10-069-056-7.rni

EATURE: |AME/KEY: exon |OCATION: 215819..215975 |YTHER INFORMATION: exon Rbis complement g34872 gene AAME/KEY: exon JOCATION: 216661..216952 OTHER INFORMATION: exon Qbis complement g34872 gene TAME/KEY: misc feature OCATION: 65854..67854 THER INFORMATION: 3'regulatory region g35018 gene KEY: misc feature TION: 213818..215818 ? INFORMATION: 3'regulatory region g34872 gene WAME/KEY: exon LOCATION: 217027..217061 OTHER INFORMATION: exon Q1 complement g34872 gene AME/KEY: exon OCATION: 215819..215941 WHER INFORMATION: exon R complement 934872 gene IANE/KEY: exon OCCATION: 216661..217061 OTHER INFORMATION: exon Q complement g34872 gene AAME/KEY: exon LOCATION: 229547..229742 OTHER INFORMATION: exon X complement g34872 gene FEATURE:
NAME/KEY: exon
COCATION: 230408.230721
OTHER INFORMATION: exon P complement g34872 gene NAME/KEY: exon LOCATION: 29388..29502 OTHER INFORMATION: exon D g35018 gene FEATURE: NAME/KEY: exon LOCATION: 29967..30282 OTHER INFORMATION: exon E g35018 gene FEATURE:
NAME/KEY: exon
LOCATION: 64666..64812
OTHER INFORMATION: exon F 935018 gene AME/KEY: exon OCATION: 201188..201234 THER INFORMATION: exon S 935030 gene /KEY: exon IION: 215702..215746 RINFORMATION: exon U 935030 gene KEY: exon ION: 216836..216915 INFORMATION: exon V 935030 gene OCATION: 65505..65853 THER INFORMATION: exon G 935018 gene /KEY: exon IION: 214676..214793 R INFORMATION: exon T 935030 gene NAME/KEY: exon OCATION: 94124..94964 OTHER INPORMATION: exon 935017 OTHER INFORMATIC FEATURE: NAME/KEY: exon

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DB 4; Length 319608;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: exon
LOCATION: 240528..240569
OTHER INFORMATION: exon M1117 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 240528..240596
JTHER INFORWATION: exon M1090 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 240528..240617
OTHER INFORMATION: exon M1069 complement g34872 gene
LOCATION: 231272..231412
OTHER INFORMATION: exon Obis complement 934872 gene
                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: exon
LOCATION: 237406..237428
OTHER INFORMATION: exon Nbis complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 240528..240644
OTHER INFORMATION: exon MS2 complement g34872 gene PATIURE:
NAME/KEX: exon
LOCATION: 240528..240824
OTHER INFORMATION: exon M862 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 240528..240994
OTHER INFORMATION: exon M692 complement g34872 gene
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NAME/KEY: misc feature
LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory region g34872 gene
FEATURE:
NAME/KEY: misc feature
LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
LOCATION: 240800..240993
OTHER INFORMATION: exon MS1 complement g34872 gene
                                                                  NAME/KEY: exon
LOCATION: 231787..231880
OTHER INFORMATION: exon O2 complement g34872 gene
                                                                                                                                                           NAME/KEY: exon
LOCATION: 231870..231879
OTHER INFORMATION: exon 01 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
.OCATION: 239719..239807
DTHER INFORMATION: exon N2 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: exon
LOCATION: 240528..241685
OTHER INFORMATION: exon M1 complement g34872 gene
FEATURE:
                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: exon
LOCATION: 234174..234321
OTHER INFORMATION: exon O complement g34872 gene
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LOCATION: 239719.:239853
DTHER INFORMATION: exon N complement g34872 gene
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42.7%; Score 25.6; D
Best Local Similarity 77.5%; Pred. No. 11;
Matches 31; Conservative 0; Mismatches
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NAME/KEY: exon
LOCATION: 292653..292841
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WATEL/CRITICAL STATES AND COTHER INFORMATION: 931-6

OCHER INFORMATION: 99-27943-150 : polymorphic base G or C NAME/KEY: allele
LOCATION: 21672

OTHER INFORMATION: 99-27935-193 : polymorphic base G or C NAME/KEY: allele
LOCATION: 65485

OTHER INFORMATION: 99-24656-260 : polymorphic base A or G NAME/KEY: allele
LOCATION: 10708 : 99-24656-260 : polymorphic base A or G NAME/KEY: allele
LOCATION: 10708 : polymorphic base A or G NAME/KEY: allele
LOCATION: 1060876

OTHER INFORMATION: 99-24634-108 : polymorphic base A or G NAME/KEY: allele
LOCATION: 1060876

OTHER INFORMATION: 99-24634-108 : polymorphic base A or G NAME/KEY: allele
LOCATION: 1060876

OTHER INFORMATION: 99-16100-147 : polymorphic base A or G NAME/KEY: allele
LOCATION: 108957

OTHER INFORMATION: 99-16100-147 : polymorphic base A or G NAME/KEY: allele
LOCATION: 108957

OTHER INFORMATION: 99-24658-167 : polymorphic base A or G NAME/KEY: allele
LOCATION: 197163

OTHER INFORMATION: 99-24658-410 : polymorphic base A or G NAME/KEY: allele
LOCATION: 197163

OTHER INFORMATION: 99-24658-410 : polymorphic base A or G NAME/KEY: allele
LOCATION: 197163

OTHER INFORMATION: 8-300-221 : polymorphic base A or G NAME/KEY: allele
LOCATION: 200778

OTHER INFORMATION: 8-300-221 : polymorphic base A or G NAME/KEY: allele
LOCATION: 200778

OTHER INFORMATION: 8-300-221 : polymorphic base A or G NAME/KEY: allele
LOCATION: 200778

OTHER INFORMATION: 8-300-123 : polymorphic base A or G NAME/KEY: allele
LOCATION: 200778

OTHER INFORMATION: 8-300-123 : polymorphic base A or G NAME/KEY: allele
LOCATION: 200778

OTHER INFORMATION: 8-300-123 : polymorphic base A or G NAME/KEY: allele
LOCATION: 200778

OTHER INFORMATION: 8-300-123 : polymorphic base A or G NAME/KEY: allele
LOCATION: 200778

OTHER INFORMATION: 8-300-123 : polymorphic base A or G NAME/KEY: allele
LOCATION: 200778

OTHER INFORMATION: 8-300-123 : polymorphic base A or G NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: 205329
OTHER INFORMATION: 8-295-125 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8-295-248 : polymorphic base A or C
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                                                  NAME/KEY: exon
LOCATION: 246273...247802
OTHER INFORMATION: exon Z
NAME/KEY: misc_feature
LOCATION: 247803...249803
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8-252-190
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LOCATION: 244353..244561
OTHER INFORMATION: exon Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 204138
OTHER INFORMATION: 8
NAME/KEY: allele
LOCATION: 204605
OTHER INFORMATION: 8
NAME/KEY: allele
LOCATION: 204304
OTHER INFORMATION: 9
NAME/KEY: allele
LOCATION: 204304
OTHER INFORMATION: 9
NAME/KEY: allele
LOCATION: 205206
OTHER INFORMATION: 9
                                                                                                                                                                                                                                                                                                  APPLICANT: Chem. Daniel
APPLICANT: Chem. Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Bugueleret, Lydie
APPLICANT: Besioux, Laurent
TITLE OF INVENTYON: SCHIZOPHRENIA ASSOCIATED GENE, PROTEINS AND BIALLELIC MARKERS
FILE REFERENCE: 53.US15.CIP
CURRENT APPLICATION NUMBER: US/09/679,409
CURRENT FILING DATE: 2000-10-03
PRIOR FILING DATE: 1999-10-12
PRIOR PLICATION NUMBER: 09/416,384
PRIOR PLICATION NUMBER: 09/416,384
PRIOR PLICATION NUMBER: 60/166,088
PRIOR PLING DATE: 1999-110-12
PRIOR PLING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 134
                                                                             137819 GAATTTATGCTTTTCAGTGCTGGAAGCATTATAGAGGTTG 137858
                          14 GAATITITICCITITICATGCTGGAACTAIGTTAAAGTITG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 199122..201122
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LOCATION: 201123..201234
OTHER INFORMATION: exon S
                                                                                                                                                                                                                  Sequence 1, Application US/09679409
Patent No. 6555316
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AME/KEY: exon
OCATION: 201123..201560
WHER INFORMATION: exon S2
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STHER INFORMATION: exon V2

VAME/KEY: exon
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OCATION: 217671..217764
THER INFORMATION: exon V1
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LOCATION: 227655..227736
OTHER INFORMATION: exon V4
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THER INFORMATION: exon W2
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DIHER INFORMATION: exon U

NAME/KEY: exon
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INFORMATION: exon V
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LOCATION: 240440..240673
OTHER INFORMATION: exon W
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OTHER INFORMATION: exon X
NAME/KEY: exon
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OCATION: 238715..238919
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OCATION: 214676..214793
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ORGANISM: Homo sapiens
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SEQ ID NO 1
LENGTH: 319608
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US-09-679-409-1
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TITLE OF INVENTION:
FILE REFERENCE: 785
 US-09-328-352-3500/c
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APPLICANT:
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: polymorphic base A or G
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                                                  : polymorphic base A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25.6; DE
Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                      LOCATION: 210361
OTHER INFORMATION: 8-283-278 :
NAME/KEY: allele
LOCATION: 210463
OTHER INFORMATION: 8-283-176 :
NAME/KEY: allele
LOCATION: 210486
OTHER INFORMATION: 8-283-153 :
NAME/KEY: allele
LOCATION: 210486
OTHER INFORMATION: 8-283-153 :
LOCATION: 210583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: 211132
OTHER INFORMATION: 8-282-92 :
NAME/KEY: allele
LOCATION: 211247
OTHER INFORMATION: 8-281-367
                                                                                                                   NAME/KEY: allele
LOCATION: 208285
OTHER INFORMATION: 8-289-322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: 212821
OTHER INFORMATION: 8-278-289
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 77.5%;
Matches 31; Conservative
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LOCATION: 211315
OTHER INFORMATION: 8-281-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele
LOCATION: 211366
OTHER INFORMATION: 8-281-248
 OTHER INFORMATION: 8-293-130
                                  CCCATION: 206545
THER INFORMATION: 8-292-198
VAME/KEY: allele
                                                                                                                                                                     AME/KEY: allele
CCATION: 208960
WHER INFORMATION: 8-287-249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEY: allele
ION: 210879
INFORMATION: 8-282-345
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                                                                                                     8-251-322
                                                                                                                                                                                                                                                         INFORMATION: 8-287-86
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THER INFORMATION: 8-283-56
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JOCATION: 211050
THER INFORMATION:
                                                                                  COCATION: 207313
DIHER INFORMATION:
                                                                                                                                                                                                                        AME/KEY: allele
OCATION: 209123
                                                                                                                                                                                                                                                                         NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                          KEY: allele
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ION: 210979
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LOCATION: 212520
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137819 GAATTTATGCTTTTCAGTGCTGGAAGCATTATAGAGGTTG 137858

RESULT 9

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Sequence 3500, Application US/09328352

Batent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGCTGGAACTATGTTAAAGTTTGCCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 accacacrargaagcriggcriragacrecticcacretroraaagrirgaraagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 cgaraccerccaccarracrrcrrrccarcerregaarcaacaaaaacrr 213
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                                                                                                                                                                                                                                                                                                                                                                                               Score 23.8; DB 4; Length 861;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CAAGAGCCTGCAGAATTTTTGCTTTTTCATGGCTGGAACTATGTTAAAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23.8; DB 3; Length 939;
Pred. No. 14;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-09-345-468-15/c
is Sequence 15, Application US/09345468
is Patent No. 6245527
is GENERAL INFORMATION:
i APPLICANT: Busfield, S.
i APPLICANT: Jandrot-Perrus, M.
i APPLICANT: Valincherker, W.
i TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF;
i FILE REFERENCE: 7853-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Busfield, S.
Villeval, J.
Jandrot-Perrus, M.
Vainchenker, W.
VENTION: GLYCOPROTEIN VI AND USES THEREOF
NCE: 7853-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/414,453A CURRENT FILING DATE: 1999-10-07 PRIOR APPLICATION NUMBER: 09/345,468 PRIOR FILING DATE: 1999-06-30 WUMBER OF SEQ ID NOS: 24 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/345,468
CURRENT FILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-414-453A-15/c
; Sequence 15, Application US/09414453A
; Detent No. 6383779
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         ; TYPE: DNA; ORGANISM: Acinetobacter baumannii US-09-328-352-3500
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 62.7%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-345-468-15
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                                                                                                                    Length 939;
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                                                                                                                                                       17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Busfield, S.
APPLICANT: Villeval, J.
APPLICANT: Villeval, J.
APPLICANT: Jandrot-Perrus, M.
APPLICANT: Jandrot-Perrus, M.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
PILE REPRENCE: 7853-47
CURRENT APPLICATION NUMBER: US/09/414,453A
CURRENT FILING DATE: 1999-10-07
PRIOR PILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Busfield, S.
APPLICANT: Villeval, J.
APPLICANT: Villeval, J.
APPLICANT: Villeval, J.
APPLICANT: Jandrot-Perrus, M.
APPLICANT: Jandrot-Perrus, M.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REPERENCE: 7583-147, 7853-147,
CURRENT APPLICATION NUMBER: US/09/345,468
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 24
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 23.8; DE; Pred. No. 14; 0; Mismatches
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Pred. No. 14;
0; Mismatches
                                                                                                                    Score 23.8; I
Pred. No. 14;
                                                                                                                                                       0; Mismatches
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FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                        RESULT 12
US-09-345-468-14/c
; Sequence 14, Application US/09345468
; Patent No. 6245527
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il Similarity 66.7%;
34; Conservative
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Best Local Similarity 66.7
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 39.7
Best Local Similarity 66.7
Matches 34; Conservative
                                         ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-414-453A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mus musculus
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                                                                                                                Query Match
Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-414-453A-14/C
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LENGTH: 1163
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SEQ ID NO 15
LENGTH: 939
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2 CAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTT 52

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17; Indels

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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARF
TITLE OF INVENTION: NOW DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709:2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 901
LENGTH: 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCAT 57
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325 CGATACCGTCCAGCATTACTTTTCCATGGTTGGAATGAAGAAAGTCT 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 726;
                                                                                                                                                                                                                                           APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Tingley, Debora W.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla W.
TITLE OF INVENTOR: GENES EXPRESSED IN ALZHEIMER'S DISEASE FILE REFREENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
ESPC ID NO 21
LENGTH: 5708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6682888 331744.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23.4; DB Fred. No. 18; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: June 3, 2004, 00:56:20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 901, Application US/09540236
Patent No. 6673910
                                                                                                                                                               Sequence 21, Application US/09566921 Patent No. 6682888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.2%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA; ORGANISM: M.catarrhalis
US-09-540-236-901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                        GENERAL INFORMATION:
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US-09-540-236-901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-566-921-21
                                                                                                                                           US-09-566-921-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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US-10-027-632-46349/c
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1941.275 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 acaagagcctgcagaatttt.....atgttaaagtttgccatgct 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_MEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                                                                                                                                                                                                                   2, 2004, 23:14:04; Search time 141 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2995936 seqs, 2280998010 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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60
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	Description	Sequence 46349, A	Seguence 46349, A	Sequence 80814, A	Sequence 80815, A	Sequence 80814, A	Sequence 80815, A	Sequence 156, App	Sequence 156, App	Seguence 156, App	Sequence 156, App	Sequence 156, App	Sequence 1007, Ap	GENERAL INFORMATI	Sequence 1, Appli
	ID	US-10-027-632-46349	US-10-027-632-46349	US-10-027-632-80814	US-10-027-632-80815	US-10-027-632-80814	US-10-027-632-80815	US-09-825-294-156	US-09-970-966-156	US-10-212-677-156	US-10-361-811-156	US-10-369-186-156	US-10-292-798-1007	US-10-147-603-1	US-10-363-426-1
	DB	13	16	13	13	16	16	0	Q	15	16	16	16	16	12
	Query Match Length DB	501	501	438	438	438	438	396	396	396	396	396	113306	319608	1392
de	Query	45.3	45.3	44.3	44.3	44.3	44.3	42.7	42.7	42.7	42.7	42.7	42.7	42.7	42.3
	Score	27.2	27.2	26.6	26.6	26.6	26.6	25.6	25.6	25.6	25.6	25.6	25.6	25.6	25.4
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	Result No.	υ	U										υ		υ

Sequence 3339, Ap	Sequence 127, App	Sequence 3, Appli	Sequence 119183,	Sequence 119183,	Sequence 1567, Ap	Sequence 250, App	Sequence 3838, Ap	Sequence 3838, Ap	Sequence 976, App	Sequence 19214, A	Sequence 15, Appl	Sequence 43, Appl	Sequence 45, Appl	'n	e 15	43	Sequence 45, Appl	•	14,	4	31,	1216	Ġ	Sequence 283, App			Sequence 63, Appl	Sequence 184, App	20	Seguence 9356, Ap
US-10-029-386-3339	US-10-101-510-127	US-10-270-144-3	US-10-027-632-119183	US-10-027-632-119183	US-10-087-192-1567	US-10-087-192-250	US-09-938-842A-3838	US-09-938-842A-3838	US-10-087-192-976	US-09-814-353-19214	US-09-832-312-15	US-09-832-312-43	US-09-832-312-45	US-09-832-312-47	US-09-829-495-15	US-09-829-495-43	US-09-829-495-45	US-09-829-495-47	US-09-832-312-14	US-09-829-495-14	US-10-157-669-31	US-10-108-260A-1216	US-10-032-585-6431	US-10-341-961A-283	US-09-900-425A-1	US-10-079-185-1	US-10-369-022-63	US-10-310-154-184	US-10-087-192-2029	US-09-918-995-9356
15	15	15	13	16	13	13	σ	H	13	2	σ	თ	σ	6	1	11	11	17	σ	1	15	16	15	16	σ	15	13	16	13	10
564	136328	9905	1043	1043	52211	370469	2000	2000	94512	583	939	939	939	939	939	939	939	939	1163	1163	1996	3246	3276	3818	4764	4764	5703	6755	95982	477
11.7	41.3	41.0	40.7	40.7	40.7	10.7	40.0	90.0	40.0	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.3
25		24.6					24	4	24	23.8	23.8	23.8	23.8	23.8	œ.	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	8	23.8	23.8	23.8	23.6
15	16	11	18	19	20	21	22	23	24	25	56	27	28	5	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

problication No. US2002019837AA1

Sequence 46349, Application US/10027632

Publication No. US2002019837AA1

SENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE REFERENCE: 10827.129

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/189,676

PRIOR APPLICATION NUMBER: US 60/199,676

PRIOR APPLICATION NUMBER: US 60/199,83

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-10-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-38

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0

SOFTWARE: FastSEQ for Windows Version 4.0

SOFTWARE: FastSEQ for Windows Version 4.0

CRANISM: Human

US-10-027-632-46349

QUART MACCH S 32; CORSELVATIVE BO.08; Pred. NO. 5.8; Pred. NO. 5.8; PRED. CORSELVATIVE BO.08; Pred. NO. 5.8; PRED. CORSELVATIVE BO.08; PRED. NO. 5.8; PRED. P

Gaps

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Sequence 80815, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE OF INVENTION: Polymorphisms in the Human Genome

FILE SPERENCS: 108827.129

CURRENT PILING DATE: 2002-04-30

FRIOR PELING DATE: 2000-07-12

FRIOR FILING DATE: 2000-07-12

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 2000-03-29

FRIOR PELING DATE: 2000-03-29

FRIOR PELING DATE: 2000-03-29

FRIOR PELING DATE: 2000-03-29

FRIOR PLING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR PLING DATE: 1999-11-23

FRIOR APPLICATION NUMBER: US 60/146,002

FRIOR APPLICATION NUMBER: US 60/146,002

FRIOR FILING DATE: 1999-08-08

FRIOR FILING DATE: 1999-08-08

FRIOR FILING DATE: 1999-08-08

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FRIOR PLING DATE: 1999-08-08

FRIOR FILING DATE: 1999-08-08

FRIOR PLING DATE: 1999-08-08-08

FRIOR PLING DATE: 1999-18-08

FRIOR PLING DATE: 19
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
File Reference: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
PRIOR PILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 ATCCTCCATATTTTTTTTTTTTTTGGAAAAGTGTTTCAGTTTGKCA 417
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                                                                                                                                                                                                                                                                                                            Length 438;
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                                                                                                                                                                                                                                                                                                        44.3%; Score 26.6; DB 13; 68.6%; Pred. No. 9.3;
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68.6%; Pred. No. 9.3;
iive 1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 80814
LENGTH: 438
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Sequence 80814, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 68.6
Matches 35; Conservative
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Best Local Similarity
Matches 35; Conserv
                                                                                                                                   ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-80814
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US-10-027-632-80815
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                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Olymorphisms in the Human Genome FILE REFERENCE: 108827.129 (CURRENT APPLICATION NUMBER: US/10/027,632 (CURRENT APPLICATION NUMBER: US/10/027,632 (CURRENT FILING DATE: 2002-04-30 (PRIOR APPLICATION NUMBER: US 60/218,006 (PRIOR FILING DATE: 2000-07-12 (PRIOR PELING DATE: 2000-04-20 (PRIOR APPLICATION NUMBER: US 60/193,483 (PRIOR APPLICATION NUMBER: US 60/193,483 (PRIOR APPLICATION NUMBER: US 60/185,218 (PRIOR APPLICATION NUMBER: US 60/185,318 (PRIOR PILING DATE: 2000-03-24 (PRIOR PILING DATE: 1000-02-24 (PRIOR PILING DATE: 1000-02-24 (PRIOR APPLICATION NUMBER: US 60/167,363 (PRIOR APPLICATION NUMBER: US 60/166,358 (PRIOR APPLICATION NUMBER: US 60/156,358 (PRIOR APPLICATION NUMBER: US 60/156,35
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APPLICATION NUMBER: US 60/146,002
FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                       Sequence 46349, Application US/10027632; Publication No. US20030204075A9
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Publication No. US20020198371A1
GENERAL INFORMATION:
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Best Local Similarity 80.0
Matches 32; Conservative
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US-10-027-632-46349
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SOFTWARE: FASTSE
SEQ ID NO 46349
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308 ANGACAATCAAAAACATTTGCTTTNAGTGGCAGGAACACTGGTACATTTTTACTTGCT 365
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GENERAL INFORMATION:

APPLICANT: Stolk, John A.

APPLICANT: Fling, Steven P.

APPLICANT: Fling, Steven P.

APPLICANT: TILING STEVEN P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C6

CURRENT FILING DATE: 2001-10-02

NUMBER OF SEQ ID NOS: 215

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 396;
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                                                                                APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REPERENCE: 210121.484C5
CURRENT APPLICATION TOWBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
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Pred. No. 21;
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Local Similarity 63.8%; Pred. No. 21;
1es 37; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 156
LENGTH: 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 11, 30, 32, 37, 309, 332
OTHER INFORMATION: n = A,T,C or G
US-09-970-966-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                | NAME/KEY: misc_feature
| LOCATION: (1)...(396)
| OTHER INFORMATION: n = A,T,C or G
US-09-825-294-156
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Best Local Similarity 63.8%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapien
          GENERAL INFORMATION:
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Matches
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Publication No. US20030204075A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION WUMBER: US/10/027,632
CURRENT APPLICATION WUMBER: US 60/218,006
PRIOR PRIOR PELING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PELING DATE: 2000-04-20
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-80-98-99
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Pred. No. 9.3;
1; Mismatches 15; Indels
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44.3%; Score 26.6; DE
Best Local Similarity 68.6%; Pred. No. 9.3;
Matches 35; Conservative 1; Mismatches
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PLING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR PELICATION NUMBER: US 60/16,358
PRIOR PELICATION NUMBER: US 60/156,358
PRIOR PELICATION NUMBER: US 60/156,358
PRIOR PELING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-09
PRIOR PLING DATE: 1999-08-09
PRIOR PLING DATE: 1999-08-09
PRIOR PELICATION NUMBER: US 60/146,002
PRIOR PERC DE NOS: 325720
SOFTWARE: PRESEEC FOR WINDOWS VERSION 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 68.6%;
Matches 35; Conservative
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US-10-027-632-80815
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LENGTH: 438
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Sequence 156, Application US/09825294 Patent No. US20020004491A1

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2003-02-14
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CURRENT FILING DATE:
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| Publication No. US20030206918A1
| GENERAL INFORMATION:
| APPLICANT: Farmer, Gary R. |
| APPLICANT: Fling, Steven P. |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER |
| TITLE OF INVENTION: WHOSER: US/10/361,811 |
| CURRENT FAPLICATION NUMBER: US/10/361,811 |
| CURRENT FILING DATE: 2003-02-05 |
| NUMBER OF SEQ ID NOS: 293 |
| SEQ ID NO 156 |
| LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15; Length 396;
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               APPLICANT: Harlocker, Susan L.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF CVARIAN CANCER
FILE REFERENCE: 210121.484C7
CURRENT APPLICATION NUMBER: US/10/212,677
CURRENT FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 288
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030232056A1
GERREAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121,484C9
CURRENT APPLICATION NUMBER: US/10/369,186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
42.7%; Score 25.6; DB
Best Local Similarity 63.8%; Pred. No. 21;
Matches 37; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.7%; Score 25.6; 63.8%; Pred. No. 21
                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc_feature
; LOCATION: 11, 30, 32, 37, 309, 332
; OTHER INFORMATION: n = A,T,C or G
US-10-212-677-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; LOCATION: 11, 30, 32, 37, 309, 332
; OTHER INFORMATION: n = A,T,C or G
US-10-361-811-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37; Conservative
Fanger, Gary R.
                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-10-361-811-156
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US-10-369-186-156
                                                                                                                                                                                                                                                 SEQ ID NO 156
LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Sequence 1007, Application US/10292798
Publication No. US20030235833A1
GENERAL INFORMATION:
APPLICANT: SUWA, WAKKNO
APPLICANT: AKIYAMA, YUTAKN
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                               308 ANGACAATCAAAAACATTTGCTTTNAGTGGCAGGAACACTGGTACATTTTTACTTGCT 365
                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                3 AAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 113306;
                                                                                                                                                                                                                                                                                    Score 25.6; DB 16; Length 396;
Pred. No. 21;
0; Mismatches 21; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96997 ritatigatiticccigrcicigaraciaticacatageriticea 96958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25.6; DB 16;
Pred. No. 1.4e+02;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 TITITGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCA
NUMBER OF SEQ ID NOS: 293
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 156
LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-246789
PRIOR FILING DATE: 2001-6-18
NUMBER OF SEQ ID NOS: 2070
                                                                                                                                     | FEATURE:
| NAME/KEY: misc feature
| LOCATION: 11, 30, 32, 37, 309, 332
| OTHER INFORMATION: n = A,T,C or G
| US-10-369-186-156
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 63.8%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.5%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , NAME/KEY: CDS
, LOCATION: (112891)..(113106)
US-10-292-798-1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
(11526)..(12452)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (37954)..(38097)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (98732)..(98784)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 084335/166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)..(113306)
                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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PERTURE:
NAME/KEY: allele
LOCATION: 148372
OTHER INFORMATION: polymorphic base A or C FEATURE:
NAME/KEY: allele
LOCATION: 149012
OTHER INFORMATION: polymorphic base A or G FEATURE:
NAME/KEY: allele
LOCATION: 149113
OTHER INFORMATION: polymorphic base C or T FEATURE:
NAME/KEY: allele
LOCATION: 14913
OTHER INFORMATION: polymorphic base C or T FEATURE:
NAME/KEY: allele
LOCATION: 151637
OTHER INFORMATION: deletion G FEATURE:
NAME/KEY: allele
LOCATION: 151748
OTHER INFORMATION: deletion G FEATURE:
NAME/KEY: allele
LOCATION: 151748
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LOCATION: 151769
OTHER INFORMATION: polymorphic base A or G
FEBTURE:
NAME/KEY: allele
LOCATION: 151847
OTHER INFORMATION: polymorphic base C or T
FEATURE:
                                                                                                                                                                                                                                                                                                                                                         MANE/KEY: allele
LOCATION: 129789
LOCATION: 129789
COTHER INFORMATION: polymorphic base C or G
FEATURE:
NAME/KEY: allele
LOCATION: 130777
OTHER INFORMATION: polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 136942..136944
OTHER INFORMATION: deletion ATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: allele
LOCATION: 146668
LOCATION: 146668
LOCATION: 14668
NAME/KEY: allele
LOCATION: 147281
COHER INFORMATION: polymorphic base C or T
CHER INFORMATION: polymorphic base C or T
FEATURE:
NAME/KEY: allele
CACATION: 120573
OTHER THFORMATION: polymorphic base A or
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele
LOCATION: 143839
OTHER INFORMATION: polymorphic base A or
                                                                                                                    NAWE/KEY: allele
LOCATION: 121527
OTHER INFORMATION: polymorphic base A
                                                                                                                                                                                                                                                                       LOCATION: 126105
OTHER INFORMATION: polymorphic base C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 147505
OTHER HIFORMATION: polymorphic base G
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 148183
OTHER INFORMATION: deletion T
                                                                                              APPLICANT: COHEN, Daniel
APPLICANT: COHEN, Daniel
APPLICANT: COHEN, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenkev, 1194
APPLICANT: Chumekev, 1194
APPLICANT: Blumenkev, 1194
APPLICANT: Blumenkev, 1194
APPLICANT: Blumenkev, 1194
APPLICANT: Braidan, Bernard
APPLICANTON NUMBER: US/10/147,603
CURRENT APPLICATION NUMBER: US 60/126,903
PRIOR APPLICANTON NUMBER: US 60/126,903
PRIOR PLING DATE: 1999-03-30
PRIOR PLING DATE: 1999-04-30
PRIOR PLING DATE: 1999-04-30
PRIOR PLING DATE: 1999-07-14
PRIOR PLING DATE: 1999-07-14
PRIOR APPLICANTON NUMBER: US 60/146,453
PRIOR APPLICANTON NUMBER: US 60/146,453
PRIOR APPLICANTON NUMBER: US 60/146,453
PRIOR PLING DATE: 1999-07-29
PRIOR PLING 
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NAME/KEY: allele
LOCATION: 112468
OTHER INFORMATION: polymorphic base G or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
ANME/KEY: allele
COCATION: 119526
OTHER INFORMATION: polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
ADME/KEY: allele
ACCATION: 111978
OTHER INFORMATION: polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OCATION: 118972
WHER INFORMATION: polymorphic base C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: allele
LOCATION: 119321
OTHER INFORMATION: polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: 110222
OTHER INFORMATION: polymorphic base G or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: allele
LOCATION: 119316
OTHER INFORMATION: polymorphic base C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: allele
LOCATION: 117324..117327
OTHER INFORMATION: deletion ACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VALUE:
NAME/KEY: allele
LOCATION: 119160..119161
OTHER INFORMATION: deletion TT
                                                                                           GENERAL INFORMATION:
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us-10-069-056-7.rnpb

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Sequence 3339, Application US/10029386
Publication No. US20030194704A1
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: HUMBALLONGEN CONTROLL OF TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GITTLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DAVE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARES Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 3339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 AAGGACAGGAAGAATATTTTTTTTTCATGTTTTGGAGCTATGCCAAGGTGTTATTTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447 cerceagaagrerrecrrreceregaagaareraaagaarecegaere 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 CCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATG 58
                                                                                                                                                                                                                                                                                                                                                                                                       Score 25.4; DB 12; Length 1392;
Pred. No. 38;
0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATURE:
COTHER INFORMATION: MAP TO CHRI7.1
COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.62
COTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.57
COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.57
COTHER INFORMATION: SWISSPROT HIT: Q9PDP1, EVALUE 7.00e+00
COTHER INFORMATION: NT HIT: AP080508.1, EVALUE 3.40e-02
COTHER INFORMATION: EST_HUMAN HIT: BE082725.1, EVALUE 8.00e-41
US-10-029-386-3339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.7%; Score 25; DB 15; Length 564;
64.9%; Pred. No. 40;
.ive 0; Mismatches 20; Indels
PPLICANT: Dohrmann, Cord
ITLE OF INVENTION: Novel Functions For DP214
                                     FILE REFERENCE: 2923-530
CURRENT APPLICATION NUMBER: US/10/363,426
CURRENT FILING DATE: 2003-02-28
FRIOR APPLICATION NUMBER: PCT/EP01/10076
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
LENGTH: 1392
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 68.6%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 64.9
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: chicken embryos
US-10-363-426-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 319608;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25.6; DB 16;
Pred. No. 2e+02;
0; Mismatches 9;
                   OCATION: 152691
THER INFORMATION: polymorphic base A or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: polymorphic base A or
                                                                                  NAME/KEY: allele
LOCATION: 152766
OTHER INFORMATION: polymorphic base A
FEATURE:
                                                                                                                                                                                   NAME/KEY: allele
LOCATION: 153046
OTHER INFORMATION: polymorphic base
                                                                                                                                                                                                                                                                               ANNE/KEY: allele
LOCATION: 153123
DTHER INFORMATION: polymorphic base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: 157238
OTHER INFORMATION: polymorphic base
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OTHER INFORMATION: polymorphic base
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THER INFORMATION: polymorphic base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 154918
OTHER INFORMATION: polymorphic base
                                                                                                                                                                                                                                                                                                                                                                                                       JOCATION: 153925
WHER INFORMATION: polymorphic base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymorphic base
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NAME/KEY: allele
CCCATION: 156448
OTHER INFORMATION: polymorphic base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.5%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAME/KEY: allele
LOCATION: 155802
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AME/KEY: allele
LOCATION: 154502
THER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 154677
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: allele
LOCATION: 158172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EATURE:
AME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 157897
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Search completed: June 3, 2004, 03:14:07 Job time : 143 secs

137819 GAATITATGCTTTTCAGTGCTGGAAGCATTATAGAGGTTG 137858

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RESULT 14
US-10-363-426-1/c
Sequence 1, Application US/10363426
Publication No. US20040072773A1
GENERAL INFORMATION:

14 GAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTG

23

26.8 44.7 736 28 BZ099915 26.6 44.3 610 28 CC163180 26.6 44.3 919 29 CG002247 26.4 44.0 529 13 BQ518948 26.4 44.0 561 28 BH167726	26.4 44.0 572 12 BM407497 26.4 44.0 577 13 BOS18947 26.2 43.7 555 9 AL798699 26.2 43.7 846 13 BX722972 26.2 43.7 845 13 BX722972 26.2 43.7 853 13 BX722662	17 26.2 43.7 890 13 BX722897 18 26.2 43.7 894 13 BX718661 19 26.2 43.7 930 29 CG334320 20 26.2 43.7 144 28 CC188331 21 26.3 43.7 144 28 CC188331	26 43.3 511 28 B37676 26 43.3 634 29 CE114130 26 43.3 709 29 CE175186	26 43.3 852 28 BZ134210 25.8 43.0 428 13 BU094768 25.8 43.0 533 12 BM902491	29 25.8 43.0 53.7 12 BM884533 30 25.8 43.0 654 29 AG046205 31 25.8 43.0 775 28 BH691334 32 25.8 43.0 775 28 BH691334	C 34 25.6 42.7 393 29 CEL101438 CEL101438 tigr-gss- C 35 25.6 42.7 410 14 CD188322 CD188322 MSI-0062P C 36 25.6 42.7 432 14 CD188324 CD188324 MSI-0062P 37 25.6 42.7 655 13 EX101851 BX101851 BX101851 38 25.6 42.7 675 29 CNSO5AFD AG164724 AG164724 Pan trogl	25.4 42.3 325 28 AZ777859 25.4 42.3 391 28 CCI73290 25.4 42.3 422 28 CCI66192 25.4 42.3 425 28 CC058194 25.4 42.3 425 28 CC166191 25.4 42.3 465 10 BEL50479	ALIGNMENTS	NX163231/c ACUS BX163231 CAPPATHOR GSS OURGANISM Danio rerio (zebrafish) CORGANISM Danio rerio BX ACTIOPLETYGIi, NeopterYgii; Teleostei; Ostariophysi; CYPTINIfORTMES; CYPTINIdae; Danio. CYPTINIfORTMES; CYPTINIDAE; BX163231 CYPTINIE DANIO.	Aumpuray, .o., nuchie, b. and Direct Submission Submitted (13-MAR-2003) The S Campus, Hinkton, Cambridgeshi humonerv@sanger.ac.uk Unoubli	rce
GenCore version 5.1.6 c 6 (c) 1993 - 2004 Compugen Ltd. c 8	ing sw model  18:15:21 ; Search time 1499.5 Seconds  (without alignments)  1194.886 Million cell updates/sec  1 5	gaattttatgttaaagtttgccatgct 60 18 19 19 c 20 c 20		1086n parameters: 55025578 27 27 27 28 28 28	33108		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	*:** *:Cun;	R R B A B A B A B A B A B A B A B A B A	results predicted by chance to have a to the score of the result being printed, of the total score distribution.	ID   Description   FEATU   FEATU   FEATU   FEATU   FEATU   GASS1810   GGSS51810   GGSS51
	OM nucleic - nucleic search, Run on: June 2, 200 Title:	t score: 60 ce: 1 g table: II	Searched: 27513289 sec	ed 1	Post-processing: Minimum Mat Maximum Mat Listing fi	Database : EST:* 1: em_estba:* 2: em_esthum: 3: em_estin:* 4: em_estmu:* 5: em_estcut:*	6: em_estp 7: em_estr 8: em_htc: 9: gb_est1 10: gb_est: 11: gb_est: 12: gb_est:	13: gb_eat 14: gb_eat: 15: em_eat:	16: em_gstenn:* 17: em_gstenn:* 18: em_gstennum:* 19: em_gste_pln:* 20: em_gste_pln:* 21: em_gste_mun:* 22: em_gste_mun:* 23: em_gste_mun:* 24: em_gste_mun:* 25: em_gste_mun:* 26: em_gste_mun:* 27: em_gste_mun:* 28: em_gste_mun:* 29: em_gste_mun:* 20: em_gste_mun:	Pred. No. is the number of a score greater than or equal and is derived by analysis o	Result Query No. Score Match Length DB c 1 30.2 50.3 806 2: c 2 28.8 48.0 543 2: 3 28.4 47.3 617 1: 4 28 46.7 668 2:

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tracking errors.
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Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG457270 617 bp mRNA linear EST 19-MAR-20
NF100H01PL1F1014 Phosphate starved leaf Medicago truncatula cDNA
clone NF100H01PL 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 543)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
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methylation filtered genomic DNA library"
                                                                                                                                                                                   223 ACAAGGGTATGCAGGACTGTTACCTTACTTAGCTGGAACTATTTCAAGTT 173
                                                                                                                                                             1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTT 51
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                                                                                    ch 50.3%; Score 30.2; DB 29; Length 806; 1 Similarity 74.5%; Pred. No. 33; 38; Conservative 0; Mismatches 13; Indels 0
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/clone="DKEY-145E6"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"
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Class: sheared ends.
Location/Qualifiers
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Fax: 301-838-0208
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/dev_stage="trifoliate"
/dev_stage="trifoliate"
/dev_stage="trifoliate"
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truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission

Submitted (12-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:si81-45-503-9111, Fax:81-45-503-9170)

Glones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Pan troglodytes DNA, clone: PTB-071D03.F, genomic survey sequence.
AG076861
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                         Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library Unpublished (2000)
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Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                      Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7325
Fax: 580 221 7380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mjharrison@noble.org
Insert Length: 617 Std Error: 0.00
Plate: 100 row: H column: 01
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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Pan troglodytes
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us-10-069-056-7.rst

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Best Local Similarity 66.7
Matches 38; Conservative
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CC163180/c
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CH230-237F3.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-237F3, genomic survey sequence.
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/clone_lib="CHORI-230 Segment 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shatsbartsbern,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M. Rat BAC End Sequences from Library CHORI-230 EçoRI segment
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                 392 GACCCTGCAAAACTTTCTCCTTTGCCAGCTGGCACAATGTTAACCTTTGTCA 443
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                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                               /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                46.7%; Score 28; DB 29; Length 668; 71.2%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other GSSB: CH230-237F3.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
                                                                                                                               /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-071D03.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10116"
/clone="CH230-237F3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Norway rat)
                                                                                           Location/Qualifiers
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                                    : pKS145
Sequencing: -21M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BZ099915.1 GI:23740799
                                                                             SacI
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                                                                                                                                                                                                                                                                                                                                                      37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           norvegicus
                                                                                                                   1. .668
                                                    R.Site 1
R.Site 2
                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 37; Conserv
                                      Vector
              LIBRARY
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                                                                                             PEATURES
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604 bp DNA linear GSS 29-APR-2003 ii60910.b2 WGS-ZmayBF (DH5a methyl filtered) Zea mays genomic clone CC163180.
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/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with Xba! and one nucleoride was added by fill in the recessive 3' end. The ganomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and ware cloned into the vector (:x/y reads in Mi3mply. .b/g reads in pUCl9). The same ligation was transformed into DHSa."
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 604)
Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,
Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L.,
Zutavern, T., McCombe, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
CHORI-230 Rat (BN/SBNH8d/MCW) BAC library produced by
Pieter de Jong"
                                                                                                                                                                         Gaps
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                                                                                                                   Length 736;
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                                                                                                                                                                                                                                54
                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
Contact: W. Richard McCombie
Contact: W. Richard McCombie
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Par: 516 367 8884
Pax: 516 367 8874
                                                                                                             Score 26.8; DB 28;
Pred. No. 3.7e+02;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.3%; Score 26.6; DB 28;
66.7%; Pred. No. 4.3e+02;
iive 0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
mol type="genomic DNA"
/cultivar="B73"
/db xref="taxon:4577"
/clone="li60g10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          604.
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Seg primer: -21M13UnivFwd
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab host="DH5a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC163180.1 GI:30190472
GSS.
                                                                                                             Query Match
Best Local Similarity 73.9%;
Matches 34; Conservative
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BH167726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
CG002247
919 bp DNA linear GSS 19-AUG-2003 ZUAAM63TV ZM_3.0_4.0_KB Zea mays genomic clone ZMMBPa0007L05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4577"
/clone=lib="zMBPa0007L05"
/clone=lib="zM_3.0_4.0_KB"
/note="Voctors: pBGSk-; Site_1: HincII; 3.4 kb 'unfiltered'
genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 529)
Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Kestrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation of a set of potato cDNA clones for microarray analyses uppublished (2002)
Other ESTS: EST626362
Context: Robin Buell
The Institute for Genomic Research
The Institute for Genomic Research
Email: potato-array@ligr.org
This clone can be obtained from the University of Arizona Genomics
                                                                                                                                                Eukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD calde; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 919)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Cliek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Other GSSs: ZUAAM63TH
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  751 AGATICTACIGIGIATITITATITIACAIGITIGGAAGGITAAATITITIGCIATACT 695
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0
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Pred. No. 4.2e+02;
0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                 genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ518948.1 GI:21377817
                                                                             CG002247.1 GI:33871666
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Class: sheared ends.
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                                                                                                                    Zea mays
                                                                                                                                      Zea mays
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BQ518948/c
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1 (bases 1 to 561)
Towkins, J.P., Peterson, D.G., Main, D., Yang, T.J., Ablett, E.F.,
Towkins, J.P., Peterson, D.G., Maters, D. and Wing, R.A.
Development of Genomic Resources for Grape (Vitis vinifera L.): BAC
library construction, preliminary STC analysis, and Identification
of Clones Associated With Flavonoid and Stilbene Biosynthesis
Unpublished (2001)
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VV_SBa0001E02f Grape Vitis vinifera genomic clone VV_SBa0001E02f,
                                                                                                                                                                                                                                                                                                                                                                                                  microarray analyses mixed potato tissues"
//note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
/Not; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating
eyes, tubers, or roots."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vitis vinifera
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, Vitaceae, Vitis.
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/note="Vector: pCUGIBAC-1; Site_1: HindIII; Site_2: NotI;
For more details on library preparation and sequence
                                                                                                                                                                                                                                                                                                                                                                         'clone_lib="Generation of a set of potato cDNA clones for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
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Institute, Orders can be made through URL: http://genome.arizona.edu/orders/
Seg primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 GAATITITICCTITICATGCCTGGAACTATGTTAAAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wing RA.
Clemson University Genomics Institute
Clemson University
To Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                         /mol_type="mRNA"
/cultivar="Kennebec or Binjte"
                                                                                                                                l. .529
/organism="Solanum tuberosum"
                                                                                                                                                                                                                                                 /db xref="taxon:4113"
/clone="STMJN06"
/tissue_type="mixed tissues"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:29760"
/clone="VV_SBa0001E02f"
/tissue_type="Young leaves"
/lab_host="E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Vitis vinifera"
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 419.
Location/Qualifiers
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/strain="Syrah"
                                                                                    cocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic survey sequence.
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Query Match Best Local (

ORIGIN

Matches

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REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

FEATURES

DEFINITION

RESULT 10 BM407497 ACCESSION VERSION

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; sateritds; lamilds; Solanales; Solanaceae; Solanum.

1 (Dases 1 to 577)

2 (Dases 1 to 577)

3 Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Karamycheva, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)

4 Other ESTS: ESTS6283

5 Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNS02F8M 1970viridis genome survey sequence T7 end of clone 132A17 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: KhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
EST626362 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMJN06
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Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472 GATTICTCCATTCCAGGCCTCGAACTATATTAGTGTTTGCCAT 515
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. 5e+02;
11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec or Binjte"
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/lab_host="SOLR"
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clone="STMJN06"
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AL194719.1 GI:7832825
GSS; genome survey sequence.
Tetraodon nigroviridis
                                                                                                                                                                 Solanum tuberosum (potato)
                                                                                BQ518947
BQ518947.1 GI:21377816
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                                                       mRNA sequence.
                                                                                                                                                                                          tuberosum
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CNS02F8M
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//clome_lib="potato roots"
//note="vector: pBluescript SK(-); Site_l: BcoRI; Site_2:
//note="vector: pBluescript SK(-); Tankeley lab;
sequencing: The Institute for Genomic Research. Roots were
isolated from in vitro grown stem cuttings on CM medium.
Roots were isolated two weeks after placing the stem
cuttings from in vitro grown plants on medium."
                         http://www.genome.clemson.edu/projects/stc/grape/VV_SBa To
order clones from this library see
http://www.genome.clemson.edu/orders"
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This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
                                                                                                                                                                                                                                                                                                  177 ACACGACCTTGAGGAATTTGTGATTCTATTAGCAAGAACTGTGTTCAAGTAACTTTTGCT 236
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van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Ake
Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.
Tanksley, S. and Baker, B.
Generation of ESTs from potato roots
Uppublished (2001)
Contact: Robin Buell
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Pred. No. 5e+02;
0; Mismatches 11; Indels 0
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/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
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Pred. No..5e+02;
0; Mismatches 21; Indels
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/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cPRO31114"
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  analysis see
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1 Similarity 75.0%;
33; Conservative (
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1 Similarity 65.0%;
39; Conservative
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Estimate of human gene number provided by genome-wide analysis

TITLE

EST 07-MAR-2003

linear

mRNA

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BQ518947

RESULT 11 BQ518947 LOCUS

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us-10-069-056-7.rst

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Sequencing primer: SP6.
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                                                                                                                                                                                                                                                                                                                                                 Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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Email: trop@sanger.ac.uk
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
BCoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 3' end and NotI at the 3' end.
Vector: pCS107; Site.l: ECORI; Site_2: NotI
HOST: ESCHERICHIA COLI DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Silurana tropicalis (western clawed frog)
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
1 (bases I to 555)
1 (bases I to 500)
2 (coning, M.D.R., Ashuret, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
On Jun 25, 2002 this sequence version replaced gi:21584403.
                                                                                                     Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Genoscope sequence ID : C0AG132AA09LP1~end : T7"
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Pred. No. 4.9e+02;
2; Mismatches 8; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Tetraodon nigroviridis"
/mol type="genomic DNA"
/mb xref="taxon:99883"
/clone="132A17"
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TROPICALIS_SEQUENCE_ID: TNeu112i05.plcSP6
  using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
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Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Email: trop@sanger.ac.uk
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_ENGUENCE ID: TTPA031m22.qlkT7
Sequencing primer: T7
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
cDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole
embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli DB108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pGSI07; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from Sug of poly A+ RNA from tadpole embryos. EcoRI-NotI cut cDNA was then ligated into pGSI07 with EcoRI at the 5' end and NotI at the 3' end"
                                                                                                                                    /dev_stage="neurula"
/lab_host="Escherichia_coli DH10B"
/clone_lib="XGC-neurula"
/clone_lib="XGC-neurula"
/note="Vector: pcSl07; Site_l: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pcSl07 with EcoRI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 ACCCTGCACTATCGTTTTATTTTTGGACCTATATGTAAGCGTACATGCT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 AGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26.2; DB 13; Length 846; Pred. No. 5.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
43.7%; Score 26.2; DB 9; Length 555;
Best Local Similarity 67.3%; Pred. No. 5.7e+02;
Matches 37; Conservative 0; Mismatches 18; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae; Silurana.

1 (bases 1 to 846)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. al Sanger Xenopus tropicalis EST project 2001 (11_2003) Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="tadpole (stage 35-40)"
/lab_host="E, coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Silurana tropicalis (western clawed frog) Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Silurana tropicalis"
|mol_type="mkm4"
|bxref="taxon:8364"
|clone="TTpA031m22"
'organism="Silurana tropicalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'clone lib="XGC-tadpole"
                                  /mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TNeul12i05"
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                                                                                                                                                                                                                             BX718662 BX718662 AGC-tadpole Silurana tropicalis cDNA clone TTpA041j10 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="TTpMOd1j10"
/dev stage="tadpole (stage 35-40)"
/dev stage="tadpole (stage 35-40)"
/lab_host="E.coil pullo"
/lab_host="S.coil pullo"
/clone lib="XG-ctadpole"
/note="Vector: pCS107; Site 1: ECORI; Site 2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from tadpole
embryos. ECORI-NOtI cut cDNA was then ligated into pCS107
with ECORI at the 5' end and NotI at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 853)
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
Contact: Croning MDR
Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is from a Xenopus Gene Collection (XGC) library constructed by Nigel Garrett.

CONSTRUCTED OF Drimed from 5ug of poly A+ RNA from tadpole embryos. ECORI-NOTI cut cDNA was then ligated into pCS107 with ECORI at the 5' end and NotI at the 3' end.

Vector: pCS107; Site_1: ECORI; Site_2: NotI HOST: ESChericia Coli DH10B.

Location/Qualifiers
Gaps
                                                                                               534 accerdentricerrecretratritriceacerariarerandeceracarieer 480
                                                  GCTTTTCATGCTGGAACTATGTTAAAGTTTGCCATGCT
18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinxton, Cambridgeshire, CB10 1SA, UK
Emal: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPTCALIS SEQUENCE ID: TTpA041j10.q1kT7
Sequencing primer: T7
                                                                                                                                                                                                                                                                                                                                                                                     Silurana tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
Mismatches
ö
                                                                                                                                                                                                                                                                               mRNA sequence.
BX718662
BX718662.1 GI:38391403
                                                                                                                                                                                                                                                                                                                                                                                                                  Silurana tropicalis
37; Conservative
                                                  6 AGCCTGCAGAATTTT
                                                                                                                                                                          RESULT 15
BX718662/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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Query Match 43.7%; Score 26.2; DB 13; Length 853;
Best Local Similarity 67.3%; Pred. No. 5.6e+02;
Matches 37; Conservative 0; Mismatches 18; Indels 0; Gaps
Oy 6 AGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 60

792 Accerdecacrategricerentratruriscaccrarareradeceracarieer 738

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Search completed: June 3, 2004, 00:54:05 Job time : 1504.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 28, 2004, 12:48:18; Search time 47.5 Seconds (without alignments) 118.967 Million cell updates/sec

US-10-069-056-9 Title:

1 TRACRIFAFHGWNYVKVCHA 20 Perfect score: Sequence:

**BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Gapop 10.0 , Gapext 0.5 Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04:\* 1: genesernleen Database

geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2001s:\*
geneseqp2003ss:\*
geneseqp2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

;		*			07172.500	
No.	Score	Query Match	Length	DB	ID	Description
-	120	100.0	20	4	AAY72705	Aay72705 Parvoviru
~	120	100.0	672	4	AAY72706	Aay72706 Parvoviru
٣	116	96.7	672	4	AAY72708	Aay72708 Parvoviru
4	116	96.7	672	4	AAY72710	Aay72710 Parvoviru
S	116	96.7	672	4	AAY72702	
9	116	96.7	672	4	AAY72704	
7	97	80.8	069	Н	AAP40306	Aap40306 Sequence
œ	53	44.2	1115	4	ABB71925	
σ	48	40.0	343	4	ABG23967	Abg23967 Novel hum
9	48	40.0	554	7	ADE82746	Ade82746 Terpenoid
ᅼ	48	40.0	580	7	ADE82685	Ade82685 Terpenoid
2	48	40.0	598	4	ABG23966	Abg23966 Novel hum
ņ	47.5	39.6	323	9	ABU22997	Abu22997 Protein e
4	47	39.5	54	4	AAU22127	Aau22127 Human car
κi	47	39.5	54	7	ADE46095	Ade46095 Human car
9	47	39.5	200	4	ABB62891	Abb62891 Drosophil
	47	39.5	505	4	ABB58292	Abb58292 Drosophil
80	46.5	38.8	430	4	ABB59252	Abb59252 Drosophil
o.	46.5	38.8		4	ABB66740	Abb66740 Drosophil
20	46	38.3	1283	4	ABB60594	Abb60594 Drosophil
21	46	38.3		ო	AAY44302	Aay44302 Mouse acr
22	45.5	37.9	806	ო	AAB42511	Aab42511 Human ORF
23	45.5	37.9	1307	9	AA031015	Aao31015 Human tra
24	45.5	37.9	1353	9	AAE29913	Hum
5	45	37.5	79	7	ADC96322	Adc96322 E. faeciu

Abb03412 Human mus Abu12706 Novel hum	Abb3163 Becneilen Aaw17929 Hop laten Abb93163 Herbicida	Abp69019 Human pol Aay82488 Human L-t Abh13114 Himan 4F2	Human		Abus6448 Lung canc Abj20208 Human SLC	Abj20207 Human SLC Abj20220 Human SLC	Abu05126 Human exp Abu05128 Human exp	Abu05125 Human exp Abu05119 Human exp
ABB03412 ABU12706	AAW17929 AAW17929 ABB93163	ABP69019 AAY82488 ABB12114	ABE56671 ABE58534	ABR48231 ABU56672	ABUS6448 ABJ20208	ABJ20207 ABJ20220	ABU05126 ABU05128	ABU05125 ABU05119
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500 50	306 426	481 507	507	507	507	507	507 507	507
36.7	36.7	36.7	36.7	36.7	36.7	36.7	36.7	36.7
4 4 4	r 4 4	4 4 4 4 4 4	4 4	44	4 4 4 4	4 4 4	4 4 4 4	4 4 4
26 27	3 7 8 3 7 8 8 7 8	321	1 m m 1 m m	36	3 9 8 6	40 41	4 4 3 2	44 45

### ALIGNMENTS

Parvovirus non-structure protein 1 (NS1) variant (T363A) peptide. AAY72705 standard; peptide; 20 AA. (revised)
(first entry) 06-AUG-2003 31-MAY-2001 Parvovirus. Synthetic. AAY72705; 

NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.

/note= "Wild type Thr substituted with Ala; This location corresponds to position 363 of the NS1 variant (T363A) shown in AAY72706" Location/Qualifiers 3 Key Misc-difference EP1077260-A1.

21-FEB-2001

99EP-00115161. 13-AUG-1999;

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM. 99EP-00115161 13-AUG-1999;

Rommelaere J; Nueesch J,

WPI; 2001-212717/22.

N-PSDB; AAD02800.

Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.

Disclosure; Page 19; 41pp; English.

The present sequence is a peptide fragment of parvovirus non-structure protein 1 (NS1) variant (T363A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the

. 361 TRACRIFAFHGWNYVKVCHA 380

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is parvovirus non-structure protein 1 (NSI) variant (T363A). The invention relates to the variants of the parvovirus non-structure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                  NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 672;
                                                                                                                                                                                                                                                                                                                                                                     /note= "Wild type Thr substituted with Ala"
                                                               Length 20;
                                                                                      0; Indels
                                                                                                                                                                                                                                                             Parvovirus non-structure protein 1 (NS1) variant (T363A).
                                                                100.0%; Score 120; DB 4; 100.0%; Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 120; DB 4;
Best Local Similarity 100.0%; Pred. No. 7.8e-10;
Matches 20; Conservative 0; Mismatches 0;
                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                    AAY72706 standard; protein; 672 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 19-21; 41pp; English
                                                                                                           1 TRACRIFAFHGWNYVKVCHA 20
                                                                                                                       99EP-00115161
                                                                                                                                                                                                                                                                                                                                                                                                                                                         99EP-00115161
                                                                                                                                                                                                                                        (first entry)
                                                                           Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rommelaere J;
                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-212717/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD02801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 672 AA;
                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                           Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                          EP1077260-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1999;
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                                                                                                                                                                                                                             06-AUG-2003
31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-2001
                                                                                                                                                                                                                                                                                                                  Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nueesch J,
                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                         AAY72706;
                                                                Query Match
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The present sequence is parvovirus non-structure protein 1 (NS1) variant
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                                                                                                                                                                                                               NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild type Thr substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                   Parvovirus non-structure protein 1 (NS1) variant (T394A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 116; DB 4;
Pred. No. 3.2e-09;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 25-27; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                672 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRACRIFAFHGWNYVKVCHA 20
AAY72708 standard; protein; 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99EP-00115161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY72710 standard; protein;
                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nueesch J, Rommelaere J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-212717/22.
N-PSDB; AAD02803.
                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1077260-A1
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31-MAY-2001
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                                                                                                                                                                                                                                                                                       Parvovirus
                                                                                                                                                                                                                                                                                                               Synthetic
                                              AAY72708;
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AAY72710
ID AAY7
XX
AC AAY7
XX
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Gaps

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Indels

TRACRIFAFHGWNYVKVCHA 20

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Parvovirus.

Synthetic

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The present sequence is a parvovirus wild-type non-structure protein 1 (NS1). The present invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSI; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild type Ser substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.7%; Score 116; DB 4; Length 672; 95.0%; Pred. No. 3.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parvovirus non-structure protein 1 (NS1) variant (S283A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KREBSFORSCHUNGSZENTRUM
                                                     (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY72704 standard; protein; 672 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 TRICRIFAFHGWNYVKVCHA 380
                                                                                                                                                                                                                                                            Disclosure, Fig 1, 41pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRACRIFAFHGWNYVKVCHA 20
                     99EP-00115161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99EP-00115161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rommelaere J;
                                                                                           Rommelaere J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
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                                                                                                                              WPI; 2001-212717/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                 N-PSDB; AAD02797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-212717,
N-PSDB; AAD02799
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Misc-difference
                     13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DEKR-) DEUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1077260-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-FEB-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-2003
31-MAY-2001
                                                                                           Nueesch J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nueesch J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY72704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is parvovirus non-structure protein 1 (NSI) variant (T463A). The invention relates to the variants of the parvovirus non-structure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy;
                                    NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 116; DB 4; Length 672; Pred. No. 3.2e-09;
                                                                                                                                                                                   /note= "Wild type Thr substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
Parvovirus non-structure protein 1 (NS1) variant (T463A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parvovirus wild-type non-structure protein 1 (NS1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Page 30-32; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY72702 standard; protein; 672 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 TRTCRIFAFHGWNYVKVCHA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRACRIFAFHGWNYVKVCHA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumoural disease; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99EP-00115161.
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95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                            Nueesch J, Rommelaere J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Conservative
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N-PSDB; AAD02805.
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                                                                                                                                                   Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 672 AA;
                                                                                                                                                                                                                                                                                                13-AUG-1999;
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06-AUG-2003 31-MAY-2001

AAY72702;

Query Match

Matches

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Claim

21-FEB-2001

Parvovirus

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1 TRACRIFAFHGWNYVKVCHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE
                                                                                                                                                                                                           ABB71925;
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                                                                                                               RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The inventors claim an immunologically active polypeptide for the development of vaccinal immunity against parvovirus infection. Also claimed are DNA sequences wholly or partly duplicative of defined sequences. The polypeptides are used in vaccines for conferring protection against parvovirus infections in man and animals. (Updated on 24-OCT-2003 to standardise OS field)
                                                                                       The present sequence is parvovirus non-structure protein 1 (NSI) variant (S283A). The invention relates to the variants of the parvovirus nonstructure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence encoded by the double-stranded replicative form DNA of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide obtd. by recombinant DNA methods - for vaccination against parvovirus infections in man and animals.
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                             96.7%; Score 116; DB 4; Length 672; 95.0%; Pred. No. 3.2e-09; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

80.8%; Score 97; DB 1; Length 690;
Best Local Similarity 70.0%; Pred. No. 2.5e-06;
Matches 14; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein envelope; immunogen; vaccine; antigen; epitope
    transcription activities, and cytotoxic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Table II, Page 33-49; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porcine parvovirus; NADL-2 virulent strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP40306 standard; protein; 690 AA.
                                                Claim 6; Page 14-16; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 TRTCRIFAFHGWNYVKVCHA 380
                                                                                                                                                                                                                                                                                                                                                                                                                            1 TRACRIFAFHGWNYVKVCHA 20
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84US-00567968,
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Best Local Similarity 95.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                       Sequence 672 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JAN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JAN-1984;
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12-JAN-1992
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AAP40306
AAP40306
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ACA AAP4
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 42567.
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                                                                                                                                                                                       ABB71925 standard; protein; 1115 AA.
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362 TRTCKIFSMHNWNYIKVCHA 381
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recombinant production of (II). The polynucleotides are also used and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal crivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for generation expression of their traits to assess blodiversity and to cid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                      Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 54326; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                        Tang YT;
                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS88154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 343 AA;
                                                                                                                              WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity.
                                                                                     Homo sapiens
                                                                                                                                                                        11-OCT-2001.
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Gaps ö 40.0%; Score 48; DB 4; Length 343; 6; Indels Pred. No. 37; 2; Mismatches 2 RACRIFAFHGWNYVKVCH 19 55.6%; Best Local Similarity 55.6 Matches 10; Conservative Query Match 8

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ADE82746 standard; protein; 554 AA (first entry) 29-JAN-2004 ADE82746; RESULT 10 

Terpenoid biosynthesis related H64 strawberry protein #27.

isoprenoid; bio-active compound synthesis; pesticide; dermatological;

cytostatic; immunosuppressive; virucide; flavour; fragrance; bio-control agent; food additive; food industry; pest control; degreasing solvent; plasticizer; dye carrier; dental caries; dental plaque; skin disorder; immunosuppressive; anti-leukaemia; anti-retroviral; monoterpene alcohol linalooi; sesquiterpene alcohol nerolidol; monoterpenoid; strawberry. virucide; flavour; fragrance

Fragaria x апапавва.

EP1231273-A1.

14-AUG-2002

12-FEB-2001; 2001EP-00200488.

12-FEB-2001; 2001EP-00200488.

(PLAN-) PLANT RES INT BV

Bouwmeester HJ Aharoni A, Verhoeven HA, Jongsma MA,

WPI; 2003-879727/82.

Novel recombinant nucleic acid encoding proteinaceous molecule, useful for producing flavor, fragrance and/or biocontrol agent which is useful as food additive in processed food industry and as antimicrobial agent.

Disclosure; Page; 52pp; English

recombinant isopremoin activities compound synchesis incience actu and its protein have the following activities; pesticide, dermatological, cytostatic, immunosuppressive, and virucide. The novel recombinant isopremoid bio-active compound synthesis mucleic acid is useful for producing flavour, fragrance, and/or a bio-control agent, by transforming or transfecting a suitable host with the recombinant isopremoid bio-active compound synthesis mucleic acid in the presence of a suitable substrate, and optionally isolating the formed product. The bio-control agent is useful as an anti-incrobial agent, as a food additive in the processed food industry to modify the taste of syrups, ince-creams, frozen desserts, yogurts, confectionery and like products, as a flavouring agent for oral medications and vitamins, and for providing additional flavour/aroma in beverages, including alcoholic beverages. The bio-control agent is also useful for enhancing or reducing flavour, control agent is also useful for the industrial synthesis of nature identical flavour/aroma substances and/or artificial flavour/aroma substances and/or artificial flavour/aroma substances and/or artificial flavour/aroma substances and/or artificial flavour/aroma in control of the interaction between plants and insects and/or plants and microorganisms, for providing flavour/aroma in products, hair conditioners, cleaning products, personal care products and health care products, as cell products and health care products, as conditions and in the preparation of a composition. The novel fracmatic in the preparation of a definition of the novel the products and health care products, and or its processed to the product of t acid is useful for the production of an antagonist e.g. an antibody or the first state of the production of an antagonist e.g. an antibody or the first state of the superior of an antagonist e.g. an antibody or the bio-control agent, useful for augmenting the synthesis of the aroma and/or taste of food or non-food products, and/or protection of food or non-food products against fungal contamination and/or prest infestation. The composition is also useful for the biological control of pests, for the protection of stored products and for the prevention or treatment of disease. The bio-control agent is useful as a degreasing solvent, plasticizer and dye carrier. The composition is useful for replacing potentially carrinogenic synthetic food additives currently capable of isoprenoid bio-active compound synthesis when provided with a suitable substrate under appropriate reaction conditions. The novel recombinant isoprenoid bio-active compound synthesis nucleic acid and its fragments is useful as a molecular marker or diagnostic tool. The protein of the novel recombinant isoprenoid bio-active compound synthesis nucleic replacing potentially carcinogenic synthetic food additives currently used. The composition is also useful for treating dental caries, dental plaque and skin disorders, and for immunosuppressive, anti-leukaemia and The invention relates to a novel isolated or recombinant nucleic acid or encoding a proteinaceous molecule essentially functional fragment,

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The invention relates to a novel isolated or recombinant nucleic acid or capable of isoprenoid bio-active compound synthesis when provided with a suitable substrate under appropriate reaction conditions. The novel recombinant isoprenoid bio-active compound synthesis mucleic acid and its protein have the following activities; pesticide, dermatological, cytostatic, immunosuppressive, and virucide. The novel recombinant isoprenoid bio-active compound synthesis nucleic acid and its producing flavour. Iragarance, and virucide. The novel recombinant producing flavour. Iragarance, and/or a bio-control agent, by transforming or transfecting a suitable host with the recombinant isoprenoid bio-active compound synthesis nucleic acid, expressing the recombinant
                compound synthesis nucleic acid or its protein is useful for the synthesis of monoterpene alcohol linalool and sesquiterpene alcohol nerolidol, and monoterpenoid. This sequence represents an H64 protein used in the terpenoid biosynthesis method of the invention. NoTE: This sequence is not shown in the specification. It has been obtained from electronic data supplied with this specification from the European Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isoprenoid bio-active compound synthesis nucleic acid in the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vel recombinant nucleic acid encoding proteinaceous molecule, useful recombing flavor, fragrance and/or biocontrol agent which is useful food additive in processed food industry and as antimicrobial agent.
anti-retroviral treatment. The novel recombinant isoprenoid bio-active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isoprenoid; bio-active compound synthesis; pesticide; dermatological; cytostatic; immunosuppressive; virucide; flavour; fragrance; bio-control agent; food additive; food industry; pest control; degreasing solvent; plasticizer; dye carrier; dental caries; dental plaque; skin disorder; immunosuppressive; anti-leukaemia; sesquiterpene alcohol nerolidol; monoterpenoid; strawberry.
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                          8,
                                                                                                                                                                                                                       DB 7; Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Terpenoid biosynthesis related H64 strawberry protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bouwmeester HJ;
                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                     Score 48; DB 7
Pred. No. 59;
7; Mismatches
                                                                                                                                                                                                                                                                                                                            357 SCKVYQKHGWNPLQSLKISWASLCNA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aharoni A, Verhoeven HA, Jongsma MA,
                                                                                                                                                                                                                                                                                                 ---YVKVCHA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE82685 standard; protein; 580 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-FEB-2001; 2001EP-00200488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-FEB-2001; 2001EP-00200488.
                                                                                                                                                                                                                     40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                          Best Local Similarity 26.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                     3 ACRIFAFHGWN-----
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                                                                                                                                                                                Sequence 554 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE82685;
                                                                                                                                                                                                                       Query Match
                                                                                                                                       Office.
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c suitable substrate, and optionally isolating the formed product. The bio-control agent is useful as an anti-microbial agent, as a food addustive in the processed food industry to modify the taste of Syrups, it is e-creams, frozen desserts, yogurts, confectionery and like products, and control agent for oral medications and vitamins, and for providing additional flavour/aroma in beverages, including alcoholic beverages. The bio-control agent is also useful for enhancing or reducing flavour, aroma substances and/or artificial products, and for the industrial synthesis of nature or artificial products, and for the industrial synthesis of nature constitutions. The biological control agent is also useful as a pest control agent control agent is also useful as a pest control agent control of the interaction between plants and insects and/or plants and microorganisms, for providing flavour/aroma in consensities, oreams, un-products, and readitioners, cleaning consensities, creams, sun-products and health care products, as a molecular marker or diagnostic cool. The protein crecombinant isopremoid bio-active compound synthesis nucleic acid is useful for the production of a composition. The novel crecombinant isopremoid bio-active compound synthesis of the bio-control agent. A composition of an antibody or its functional equivalent which is useful for inhibiting the synthesis of the aroma and/or taste of food or non-food products, and don't pest the bio-control agent. A composition of a control agent is useful for the protection of stored products, and for the protection of stored products, and for the protection of stored products and for the biological control agent is useful for the protection of stored products and solution is a degressing creament, plasticiars and dye carrier. The composition is a degressing control agent is useful for the protection of stored products and suffice and stin ä compound synthesis nucleic acid or its protein is useful for the synthesis of monoterpene alcohol linalool and sesquiterpene alcohol natolidol, and monoterpenoid. This sequence represents an H64 protein used in the terpenoid biosynthesis method of the invention. NOTE: This sequence is not shown in the specification. It has been obtained from electronic data supplied with this specification from the European Patent Gaps Human, chromosome mapping, gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. 8; Score 48; DB 7; Length 580; Pred. No. 62; 4; Indels 40.0%; Scor. No. 02., 26.9%; Pred. No. 02. 383 SCKVYQKHGWNPLRSLKISWASLCNA 408 3 ACRIFAFHGWN-----YVKVCHA 20 Novel human diagnostic protein #23957. ABG23966 standard; protein; 598 AA 30-MAR-2001; 2001WO-US008631. 18-FEB-2002 (first entry) Query Match
Best Local Similarity 26.5. Sequence 580 AA; WO200175067-A2. Homo sapiens. 11-OCT-2001 ABG23966; RESULT 12 ABG23966 셤 ð

08-FEB-2002; 2002US-00072851

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal ectivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbarrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and anno acid sequences. Aggonolo-Abg30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at (IP) wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.0%; Score 48; DB 4; Length 598; 55.6%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #8524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 54325; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU22997 standard; protein; 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 RARAIVAFHGGNYRELYH 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RACRIFAFHGWNYVKVCH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                                              Tang YT
31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
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                                                                                            Drmanac RT, Liu C,
                                                                                                                               WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                      (HYSE-) HYSEQ INC
                                                                                                                                                   N-PSDB; AAS88153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 598 AA;
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ABU22997
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The invention relates to an instance and compilating any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a propose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated continued by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway continued for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene product lies correspond that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sectivity; (11) a culture compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sectivity; (11) a culture compound that inhibits the extent correction of an organism. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids required for for entil and continued for rational action of an organism. The antisense modeled acids required for for entil and continued for rational activity and activity of a compound and antisense modeled activity of a compound and activity of a compound activity activity of a compound activity activity of a compound activity activity of a compound
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                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chicken, sheep, immunosuppressive, antiarthritic, vasotropic, dog, antirheumatic, antiproliferative, cytostatic, cardiant, neuroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat;
                                                                                                                            Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                      isolate candidate molecules for rational drug discovery programs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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                                                                                                                            Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                            Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 50921; 1766pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tp.wipo.int/pub/published_pct_sequences
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                                                                                                                            Malone C,
                                                                                                                                                      Carr GJ,
                     06-MAR-2002; 2002US-0362699P.
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Matches 8; Conservative
                                                                           (ELIT-) ELITRA PHARM INC.
                                                                                                                            Zamudio C,
Trawick JD,
                                                                                                                                                                                                          WPI; 2003-029926/02
                                                                                                                                                                                                                                     N-PSDB; ACA26867
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                                                                                                                            Wang L,
Wall D,
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2000US-0234223P. 2000US-0234274P. 2000US-0234997P.

.000US-0234998P. 2000US-0235834P

2000US-0235836P. 2000US-0236327P. 2000US-0236367P.

2000US-0236368P. 2000US-0236369P. 2000US-0236370P. 2000US-0236802P.

2000US-0237037P. 2000US-0237038P. 2000US-0237039P.

2000US-0237040P 2000US-0239937P 2000US-0241221P 2000US-0241785P. 2000US-0241786P.

000US-0240960P

2000US-0241808P. 2000US-0241809P.

000US-0241826P

2000US-0244617P

000US-0246476P

2000US-0246523P

000US-0246524P

2000US-0241787P

2000US-0246538P.

000US-0246527P

000US-0246609P

2000US-0246610P. 2000US-0246611P. 2000US-0246613P.

2000US-0249208P.

2000US-0249210P

2000US-0249207P

000US-0249211P.

2000US-0249213P :000US-0249214P

2000US-0249215P. 2000US-0249216P. 2000US-0249217P.

2000US-0249218P

000US-0249265P 2000US-0249299P

2000US-0251479

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14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
27-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
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08-NOV-20001

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05-DEC-2000;
06-DEC-2000;
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L7-NOV-2000;
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17-NOV-2000;
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  cerebroprotective, nootropic; antibacterial; virucide, fungicide, cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; cerebrovascular disorder; hugal infection; fungal infection; ocular disorder; bacterial infection; fungal infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; tissue regeneration;
                                                                                                                                                                                                            16-MAR-2000; 2000US-0186150P.
16-MAR-2000; 2000US-0186150P.
11-MAR-2000; 2000US-0189874P.
11-MAR-2000; 2000US-01998123P.
19-MAY-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0198123P.
28-UN-2000; 2000US-0215135P.
30-UN-2000; 2000US-0216647P.
07-UUL-2000; 2000US-021688P.
11-UUL-2000; 2000US-021688P.
11-UUL-2000; 2000US-021688P.
11-UUL-2000; 2000US-0217496P.
11-UUL-2000; 2000US-0217496P.
14-UUL-2000; 2000US-0218290P.
26-UUL-2000; 2000US-0220868P.
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14-AUG-2000) 2000US-0225757P.
14-AUG-2000) 2000US-0225757P.
18-AUG-2000) 2000US-0225759P.
18-AUG-2000) 2000US-0226681P.
22-AUG-2000) 2000US-0226681P.
22-AUG-2000) 2000US-0227688P.
23-AUG-2000) 2000US-022934P.
01-SEP-2000) 2000US-022934P.
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05-SEP-2000) 2000US-022934P.
06-SEP-2000) 2000US-022934P.
06-SEP-2000) 2000US-022934P.
06-SEP-2000) 2000US-022934P.
06-SEP-2000) 2000US-023143P.
06-SEP-2000) 2000US-023144P.
06-SEP-2000) 2000US-023196P.
14-SEP-2000) 2000US-023196P.
14-SEP-2000) 2000US-023299P.
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14-AUG-2000; 2000US-0225513P.
14-AUG-2000; 2000US-0225213P.
14-AUG-2000; 2000US-022526F.
14-AUG-2000; 2000US-022526F.
14-AUG-2000; 2000US-022526F.
                                                                                                                                                             17-JAN-2001; 2001WO-US001340
                                                                                                                     WO200155321-A2
                                                                                                                                                                                 31-JAN-2000; 204-FEB-2000; 24-FEB-2000; 2
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                                                                                                 Homo sapiens
                                                                                                                                        02-AUG-2001
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26-SEP-2000; 2000US-0235484P
                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cardiovascular system related polypeptide; cancer; proliferative disorder; foetal abnormality; developmental abnormality; proliferative disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer; disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine disorder; pregnancy-related disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                               08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                            2000US-0251868P.
2000US-0251869P.
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ADE46095
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2000US-0224518P.
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                                                 07-MAR-2002; 2002US-00091504
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01-DEC-2000; 2000US-0250160P.
05-DEC-2000; 2000US-0250180P.
05-DEC-2000; 2000US-0251988P.
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06-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-0251868P.
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08-DEC-2000; 2000US-025189P.
11-DEC-2000; 2000US-025199P.
11-DEC-2000; 2000US-025199P.
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                                        27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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The invention relates to human cardiovascular system related polypeptides and the polynucleotides encoding them. The polypeptides, polynucleotides and antibodies to the polypeptides are useful for diagnosing a and antibodies to the polypeptides are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer of cardiovascular system tissues, proliferative disorders, foetal cand developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, cathorosclerosis, cardiovascular disorders, angiogenic disorders, atherosclerosis, cardiovascular disorders, angiogenic disorders, and infections. The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and polymucleotides are also useful for chromosome identification, radiation hybrid mapping or long-range capabilities, fat content or other mutritional components. This sequence represents a human cardiovascular system
                                                                                                                                                       New cardiovascular system related polynuclectides and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer of cardiovascular tissues and cancer metastases.
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                                                                                                                                                                                                                                                            Claim 11; SEQ ID NO 901; 262pp; English
                                            Barash SC
(HUMA-) HUMAN GENOME SCI INC.
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                                            Ruben SM,
                                                                                          WPI; 2003-743766/70.
N-PSDB; ADE45480.
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# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

May 28, 2004, 12:52:43 ; Search time 10.5 Seconds (without alignments) 183.222 Million cell updates/sec Run on:

US-10-069-056-9 Perfect score: Title:

120 1 TRACRIFAFHGWNYVKVCHA 20 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	UYPV1M	A44276	UYPVIM	UYPVV1	UYPVNA	UYPVPP	UYPV1F	UYPVCP	UYPVME	UYPVFP	T19406	D71842	C96638	G90104	T31646	T15249	T32479	T02491	JQ1250	A87602	C69771	T08550	JG0165	T11166	A88065	D44503	JC5235	JC5677	C44503	
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	Result No.	1	7	m	4	2	9	7	œ	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	

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S74431	T46355	S74473	AG0521	A96660	G85070	VCVYPV	A48549	AH3145	G72854	G71414	C98142	ODBY1	S17993	JU0148	S78640
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358	425	491	887	605	124	293	297	359	363	407	411	512	534	534	534
35.8	35.8	35.8	35.8	35.4	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0
43	43	43	43	42.5	42	42	42	42	42	42	42	42	42	42	42
0	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

- E	Σ
ESUL	IYPV1

noncapsid protein NSI - minute virus of mice
c; Species: minute virus of mice, murine parvovirus
C; Species: minute virus of mice, murine parvovirus
C; Date: 14-Nov-1983 #sequence\_revision 28-Aug-1985 #text\_change 08-Apr-1994
C; Cacessiann A03696
C; Accessiann A03696
A; Fitle: The complete DNA sequence of minute virus of mice, an autonomous parvovirus.
A; Fitle: The complete DNA sequence of minute virus of mice, an autonomous parvovirus.
A; Fitle: The complete DNA sequence of minute virus of mice, an autonomous parvovirus.
A; Fitle: The Complete DNA sequence of minute virus of mice, an autonomous parvovirus.
A; Fitle: The Complete DNA sequence of minute virus of mice, an autonomous parvovirus.
A; Fitle: The Complete DNA A; Fitle: The Comple

Gaps ö Score 116; DB 1; Length 672; Pred. No. 1.8e-10; 0; Mismatches 1; Indels Query Match 96.7%; Best Local Similarity 95.0%; Matches 19; Conservative 0

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361 TRICRIFAFHGWNYVKVCHA 380 g

#### RESULT 2

noncapeid protein NS1 - parvovirus LuIII
C;Species: A4276
R;Diffoot, N.; Chen, K.C.; Bates, R.C.; Lederma, M.
Virology 192, 339-3155, 1993
A;Title: The complete nucleoride sequence of parvovirus LuIII and localization of a uniquality and sequence number: A44276
A;Title: The complete nucleoride sequence of parvovirus LuIII and localization of a uniquality and sequence number: A44276
A;Title: The complete nucleoride sequence of parvovirus LuIII and localization of a uniquality in the sequence of parvovirus nor shown
A;Residues: 1-68 < LIF>
A;Cross-references: GB:M8188
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein

95.8%; Score 115; DB 1; Length 668; 90.0%; Pred. No. 2.6e-10; Live 1; Mismatches 1; Indels 18; Conservative Query Match Best Local Similarity Matches 18; Conserv

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Ribergeron, J.; Menezes, J.; Tijssen, P.
Virology 197, 86-98, 1993
A.Fitle: Genomic organization and mapping of transcription and translation products of the A.Fitenence number: A48472; MUID:94025614; PMID:8212598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Carlson, J.; Rushlow, K.; Maxwell, I.; Maxwell, F.; Winston, S.; Hahn, W. J. Virol. 55, 574-587, 1985
A;Title: Cloning and sequence of DNA encoding structural proteins of the autonomous parvc A;Recession: N03697; MUID:85265017; PMID:2991581
A;Accession: A03697
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-85, TR', 87-273, TR', 275-375, VV', 377-620, NLH', 623-624, PTPPD', 630, AIR', 634, '
A;Cross-references: EMBL:M38367; NID:g332987; PIDN:AAA46920.1; PID:g332989
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:D00623; NID:g303754; PIDN:BAA00501.1; PID:g222358
R;Vasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W.
Virology 178, 611-616, 1990
A;Title: The complete nucleotide sequence of an infectious clone of porcine parvovirus, A;Reference number: A36217; MUID:91021005; PMID:2219713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   noncapsid protein NS1 - porcine parvovirus (strain NADL-2)
C;Species: porcine parvovirus
C;Species: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 16-Jun-2000
C;Accession: A33302; B36217; A36217
R;Ranz, A.I.; Manclus, J.J.; Diaz-Aroca, E.; Casal, J.I.
J. Gen. Vir.O. 70, 2541-2533, 1989
A;Title: Porcine parvovirus: DNA sequence and genome organization.
A;Reference number: A33302; MUID:90010964; PMID:2794971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           noncapsid protein NS1 - feline panleukopenia virus (fragment)
C;Species: feline panleukopenia virus, FPLV
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
                          A;Molecule type: DNA
A;Residues: 1-662 <VAS>
A;Cross-references: EMBL:M38367; NID:g332987; PIDN:AAA46920.1; PID:g332989
                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-662 <BER>
A;Experimental source: strain NADL-2, ATCC VR-742
A;Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBIP:138790)
C;Superfamily: parvovirus noncapsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.8%; Score 97; DB 1; Length 662; 70.0%; Pred. No. 1.8e-07; tive 3; Mismatches 3; Indels
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Pred. No. 1.1e-06;
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65.0%; Pred. No. 1...
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                                                                                                                            A; Experimental source: strain NADL-2
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Best Local Similarity 70.0
Matches 14; Conservative
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Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A33302
A; Molecule type: DNA
A; Residues: 1-660 < RAN>
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A; Accession: A36217
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C;Species: parvovirus H1
A;Note: host Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 16-Jul-1999
C;Accession: A03695
E;Rhode III, S.L.; Paradiso, P.R.
J. Virol. 45, 173-184, 1983
A;Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybri
                                                                                noncaped protein NSI - minute virus of mice (strain NVMi)

() Species: minute virus of mice, murine parvovirus

() Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999

() Accession: A23008; A29510

R; Sahli, R.; McMaster, G.K.; Hirt, B.

Nucleic Acids Rese. 13, 317-333, 1985

A; Title: DNA sequence comparison between two tissue-specific variants of the autonomous A; Reference number: A23008; MUD:85242059; PMID:3855242

A; Accession: A23008

A; Molecule type: DNA

A; Residues: 1-721 <SAH>
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N;Alternate names: nonstructural protein NS-1
C;Species: porcine parvovirus
C;Date: 31-Dec-1990 #sequence revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: A36217; A48472; A33743
R;Vasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W.
Virology 178, 611-616, 1990
A;Title: The complete nucleotide sequence of an infectious clone of porcine parvovirus, A;Reference number: A36217; MUID:91021005; PMID:2219713
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X02481
R;Astell, C.R.; Gardiner, E.M.; Tattersall, P.
J. Virol. 57, 656-669, 1986
A;Title: DNA sequence of the lymphotropic variant of minute virus of mice, MVM(i), and A;Reference number: A29510; MUID:86115415; PMID:3502703
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A.Molecule type: DNA
A.Residues: 1-672 <RHO>
A.Cross-references: EMBD:X01457; NID:g60993; PIDN:CAA25689.1; PID:g60994; EMBL:J02198
C.Superfamily: parvovirus noncapsid protein
C.Keywords: noncapsid protein
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A.Molecule type: DNA
A.Residues: 1-645, 1', 447-721 <AST>
A.Cross-references: EMBL: M12032; NID:g332289; PIDN:AAA69566.1; PID:g825477
C.Superfamily: parvovirus noncapsid protein
C.Keywords: noncapsid protein
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Best Local Similarity 85.0.
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Arritle: Nucleotide sequence of feline panleukopenia virus: comparison with canine parvon A; Reference number: A36608; MUD:91073139; PMID:2174965
A; Accession: A36608
A; Molecule type: DNA
A; Residues: 1-668 <AAR>
A; Cross-references GB: X55115; NID:960863; PIDN:CAA38910.1; PID:960864
C; Superfamily: parvovirus noncapsid protein
C; Keywords: noncapsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dypothetical protein jhp1160 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Accession: D71842
C;Accession: D71842
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Irves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jing, Q.; Taylor, D.E.; Vovis, G.F.; J Nature J97, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathch A;Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-136 <ARN>
A;Cross-references: GB:AE001543; GB:AE001439; NID:g4155753; PIDN:AAD06732.1; PID:g4155754
A;Experimental source: strain J99
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A;Cross-references: EMBL:270034; PIDN:CAA93857.1; GSPDB:GN00020; CESP:C18E9.8
A;Experimental source: clone C18E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C18E9.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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C;Superfamily: Caenorhabditis elegans hypothetical protein C18E9.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.1%; Score 62.5; DB 2; Length 586; 75.0%; Pred. No. 0.049; cive 1; Mismatches 2; Indels
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C;Superfamily: Helicobacter pylori hypothetical protein jhp1160
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Pred. No. 1.7e-06;
4; Mismatches 3; Indels
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A;Accession: T19406
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RiSims, M. submitted to the EMBL Data Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 SRTCQIFRMHGWNWIKVCHA 381
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   Virol. 71, 2747-2753, 1990
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Best Local Similarity 65.0%;
Matches 13; Conservative '
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Best Local Similarity 75.0
Matches 12; Conservative
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Best Local Similarity
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A; Status: preliminary
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(Species: mink enteritis virus, MEV
(C)Species: mink enteritis virus, MEV
(C)Species: mink enteritis virus, MEV
(C)Sate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
(C)Accession: A38350
(R)Kariatsumari, T.; Horiuchi, M.; Hama, E.; Yaguchi, K.; Ishigurio, N.; Goto, H.; Shinag A; Gen. Virol. 72, 867-875, 1991
(A) Title: Construction and nucleotide sequence analysis of an infectious DNA clone of the A; Reference number: A38350; MUID:91202123; PMID:2016597
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C;Species: feline panleukopenia virus, FPLV
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C;Accession: A36608
R;Martyn, J.C.; Davidson, B.E.; Studdert, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             noncapsid protein NS1 - canine parvovirus (strain N)
C;Species: canine parvovirus, CPV
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: A29962
A,Residues: 1-392 <CAR>
A,Cross-references: EMBL:M10824; NID:g333474; PIDN:AAA47160.1; PID:g333475
C,Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: A29962
A;Molecule type: DNA
A;Residues: 1-668 CKEE>
A;Cross-references: EMBL:M19296; NID:g333438; PIDN:AAA67459.1; PID:g333439
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: A29962
R;Red, A.P.; Jones, B.V.; Miller, T.J.
Virol. 62, 266-276, 1988
A;Title: Nucleotide sequence and genome organization of canine parvovirus.
A;Reference number: A29962; MUID:88062992; PMID:2824850
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A;Molecule type: DNA
A;Residues: 1-66 × cARA>
A;Cross-references: GB:D00765; NID:g222435; PIDN:BAA00662.1; PID:g222436
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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                                                                                                                                                 Query Match 75.8%; Score 91; DB 1; Length 392; Best Local Similarity 65.0%; Pred. No. 9.9e-07; Matches 13; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 75.8%; Score 91; DB 1; Length 668; Best Local Similarity 65.0%; Pred. No. 1.7e-06; Matches 13; Conservative 4; Mismatches 3; Indels
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Pred. No. 1.7e-06;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                  86 SRICQIFRMHGWNWIKVCHA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 SRTCQIFRMHGWNWIKVCHA 381
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Best Local Similarity 65.0%;
Matches 13; Conservative '
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Gaps

ua-10-069-056-9.rpr

Gaps

10;

Indels

3,

4; Mismatches

Conservative

10;

Matches

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hypothetical protein Y57A10A.x - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
C;Accession: T31646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: CBSP:Y57A10A.x
A;Introns: 89/2; 244/2; 423/3
C;Superfamily: Caenorhabditis elegans hypothetical protein Y57A10A.x
                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-490 <WIL>
A;Cross-references: BMBL:AL117195; PIDN:CAB55029.1; CESP:Y57A10A.x A;Experimental source: clone Y57A10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

38.8%; Score 46.5; DB 2; Length 490;
Best Local Similarity 47.1%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                               Rismye, R. submitted to the EMBL Data Library, September 1999 submitted to the EMBL Data Library, September 1999 A; Reference number: 221048 A; Ascession: T31646 A; Status: preliminary; translated from GB/EMBL/DDBJA; Molecule type: DDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: May 28, 2004, 13:00:58 Job time: 11.5 secs
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6190104
putative tetrameric tRNA splicing endonuclease [imported] - Guillardia theta nucleomorph
cj.Species: nucleomorph Guillardia theta
A,Note: a nucleomorph Guillardia theta
A,Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C,Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C,Accession: G90104 #sequence_revision 10-May-2001 #text_change 24-May-2001
R,Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A,Reference number: A99082; WUID:11323671; PMID:11323671
A,Accession: G90104
A,Accession: G901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rithors: Salzberg, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hutzar, L.
Anture 408, 1800, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Sooney, T.; Rooney, T.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Fitle. Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F11P17.5 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C96638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 2;
Pred. No. 9.9;
4; Mismatches
                                                                                                                                              4 CRIFAFHGWN------YVKVCHA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRACRIFAF---HGWNYVKV 17
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Best Local Similarity 45.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 40.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-594 <STO>
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A, Genome: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: F11P17.5
A; Map position: 1
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RESULT 15

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May 28, 2004, 12:48:53 ; Search time 6.75 Seconds (without alignments) 154.282 Million cell updates/sec Run on:

US-10-069-056-9 120 1 TRACRIFAFHGWNYVKVCHA 20

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

					SUMMARIES	
Result		Ouerv				
No.	Score	Match	Length	DB	ID	Description.
н	116	96.7	672	н	VNCS MUMIV	1
7	115	95.8	668	н	VNCS_PAVL3	P36311 parvovirus
m	113	94.2	672	Н	VNCS MUMIM	0
4	106	•	672	-	VNCS_PAVHH	
Ŋ	97	80.8	662	Н	VNCS PAVPK	2 porcine
9	92	٠.	099	٦	VNCS_PAVPN	porcine
7	91	75.8	392	-	VNCS_FPV	
80	91	•	699	٦	VNCS_FPV19	feline
σ	91	75.8	699	ч	VNCS MEVA	8 mink en
10	91		668	٦	VNCS PAVCN	P12929 canine parv
11	48	•	246	ч	SIX6 HUMAN	095475 homo sapien
12	48	ö	246	ä	SIX6 MOUSE	_
13	46	38.3	299	н	COAT HELVS	Q00556 helenium vi
14	46	ъ.	2126	Н	PKDR_MOUSE	Q9z0t6 mus musculu
15	45.5	37.9	1310	-	A8B3_HUMAN	O60423 homo sapien
16	45	٠	315	ч	COAT_CVB	_
17	44	36.7	421	-		
18		36.7	422	Н	CHMO_ARATH	
19	44	36.7	507	7	LAT1_HUMAN	
20	44	36.7	512	7	LAT1_MOUSE	_
21	44	36.7	512	Н	LAT1_RAT	Q63016 rattus norv
22	43.5	•	521	-	PGS1_YEAST	
23	43	•	282	-	Y32K_BNYVG	
24	43	٠	396	Н	APN1_CAEEL	Q10002 caenorhabdi
25	43	35.8	491	ч	· GLG2_SYNY3	P72623 synechocyst
56	43	S		Н		
27	43	35.8	N	Н	- 1	Q9ntg1 homo sapien
28		35.4	295	Н	TYSY ZYMMO	Q92671 zymomonas m
29	42.5	35.4	521			
30		35.4	1251	-1	A8B1_HUMAN	_
31	42	35.0	238	H	ATE_SHEON	_
32	42	35.0	293	ч		
33	42	35.0	363	٦	VP43_NPVAC	_

35.0 530 1 AAA1 MOUSE Q9jmh8 mus musculu	70000 t 1000	534 I COAL KLULA	534 1 COX1_SACDO P98001	534 1 COXI_YEAST P00401	552 1 HAS2_CHICK .	571 1 SYE METAC Q8tt52	796 1 PTRA_RAT Q03348	802 1 PTRA_HUMAN P18433	829 1 PTRA_MOUSE P18052	852 1 GLNI	852 1 GLND_NEIMB Q9jzb4	ALIGNMENTS
523 1	530 1	. 534 1	534 1	534 1	552 1	571 1	796 1	802 1	829 1	852 1	852 1	
42							42				42	

ALIGNMENIS RESULT 1	VNCS_MUMIV ID VNCS MUMIV STANDARD; PRT; 672 AA.		15-DEC-1998 (Rel. 37, Last Noncapsid protein NS-1 (Nor		OS Murine minute virus (Murine parvovirus).			RP SEQUENCE FROM IN.	MEDDINE=83143341; FubMed=8298/3/; Astell C.R., Thomson M., Merchlinsky M., Ward		parvovirus.";	kb. Nucleic Acids Kes. 11:999-1018(1983). CC!- FUNCTION: Seems necessary for viral DNA replication.					use by non-profit institutions as long as its content is in no	modified and this statement is not rem	CC entities requires a license agreement (See http://www.isb-sib.ch/announce/	or send an email to incensewish-sid.or	EMBL; J02275; AAA67109.1;		DR PIR, A03696; UYPVIM.				ATP-binding.	FI NP BIND 399 406 AIF (POTENTIAL). SQ SEQUENCE 672 AA; 76248 MW; 50298F27662E3CID CRC64;	Ouerv Match 96.7%: Score 116: DB 1: Length 672;	Similarity 95.0%; Pred. No. 1.5e-10; 9; Conservative 0; Mismatches 1;	Qy 1 TRACRIFAFHGWNYVKVCHA 20			SULI Z S_PAVL3	ID VNCS PAVL3 STANDARD; PRT; 668 AA.		[
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406 ATP (POTENTIAL).
75993 MW; 12F331142F72AA6D CRC64;
                                                                                                                                                                                                                        ATP (POTENTIAL).
I -> L (IN REF. 2).
25F025FE328B4DF0 CRC64;
                                                                                                                                                                                                                                                                                      94.2%; Score 113; DB 1;
90.0%; Pred. No. 4.4e-10;
iive 1; Mismatches 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    672 AA.
                                                                                                                          EMBL; X02481; -; NOT ANNOTATED CDS. EMBL; M12032; AAA69567.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Pfam; PF01057; Parvo NS1; I.
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                                                                                                                                                          InterPro, IPR001257; Parvo NS1. Pfam; PF01057; Parvo NS1; 1.
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                                                                                                                                                                                                                                                       76140 MW;
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                                                                                                                                                                                                                                                                                                        Local Similarity 90.0
nes 18; Conservative
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672 AA;
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                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"DNA sequence comparison between two tissue-specific variants of the autonomous parvovirus, minute virus of mice.";
Nucleic Acids Res. 13:367-1985).
-i- FUNCTION: Seems necessary for viral DNA replication.
-i- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                            Virology 192:339-345(1993).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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MEDIINE=86115415; PubMed=3502703;
Astell C.R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice, MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                  Parvovirus LuIII.
Viruses; 88DNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=35339;
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Viruses; seDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10795;
                                                                                                                               MEDLINE=93297126; PubMed=8517025;
Diffeot N., Chen K.C., Bates R.C., Lederma M.;
The complete nucleotide sequence of parvovirus LulII and
"The complete unique sequence possibly responsible for its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 115; DB 1; Length 668;
Pred. No. 2.1e-10;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNCS MUMIM STANDARD; PRT; 672 AA.
P07300; P10837;
01-APR-1998 (Rel. 07, Created)
01-JUL-1999 (Rel. 11, Last sequence update)
15-DEC-1999 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A44276; A44276. — — — — — — — InterPro; IPR001257; Parvo NS1. Pfam; PF01057; Parvo NS1; I. Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TP (POTENTIAL).
CAE69049F8F86B53 CRC64;
   15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M81888; -; NOT_ANNOTATED_CDS.
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668 AA; 75846 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                encapsidation pattern.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prototype strain."
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                                                                                                                   SEQUENCE FROM N.A.
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-i. Virol. 45:173-184(1983).
-i. FUNCTION: Seems necessary for viral DNA replication.
-i. SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nonstructural protein; Noncapsid protein; DNA replication;
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85.0%; Pred. No. 5.5e-09;
ive 1; Mismatches 2; Indels
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                                                                                                                                                  SEQUENCE OF 367-660 FROM N.A. MEDLINE=90085785; PubMed=2596019; Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.; Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.; Vasudevacharya J., Basak S., Srinivas R.V., Compans H.W.; Valcotide sequence analysis of the capsid genes and the right-hand terminal palindrome of porcine parvovirus, strain NADL-2."; Virology 173:368-377(1989).
-i. FUNCTION: Seas necessary for viral DNA replication.
-i. SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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K -> R (IN REF. 2).

C -> V (IN REF. 2).

TALTQHARFSNTDT -> NLHLIPTPPDSAIRTP (IN
complete nucleotide sequence of an infectious clone of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=85265017; PubMed=2991581; Maxwell F., Winston S., Hahn Carlson J., Rushlow K., Maxwell I., Maxwell F., Winston S., Hahn "Cloning and sequence of DNA encoding structural proteins of the autonomous parvovirus feline panleukopenia virus."; J. Virol. 55:574-587 (1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feline panleukopenia virus (FPV).
Viruses; SSDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=10786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.7%; Score 92; DB 1; Length 660; 65.0%; Pred. No. 8.3e-07; Live 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         660 AA; 75300 MW;
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                                        parvovirus, strain NADL-2."
Virology 178:611-616(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 65.0 Matches 13; Conservative
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SEQUENCE FROM N.A.
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376
621
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    -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=96183900; PubMed=8642680;
MEDLINE=96183900; PubMed=8642680;
Bergeron J., Hebert B., Tijssen P.;
"Genome organization of the Kresse strain of porcine parvovirus:
identification of the allotropic determinant and comparison with
those of NADL-2 and field isolates.";
J. Virol. 70:2508-2515(1996).
-I- FUNCTION: Seems necessary for viral DNA replication.
                                                                                                                                                                                                                                                                                                                                                                                                                              Porcine parvovirus (strain Kresse) (PPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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VCBI_TaxID=10797;
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SEQUENCE FROM N.A.
MEDLINE=90100564; PubMed=2794971;
RADIANE=90100564; Manclus J.J., Diaz-Aroca E., Casal J.I.;
Ranz A.I., Manclus J.J., Diaz-Aroca end genome organization.";
"Porcine parvovirus: DNA sequence and genome organization.";
J. Gen. Virol. 70:2541-2553(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=91021005; PubMed=2219713;
Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 405 ATP (POTENTIAL).
662 AA; 75591 MW; B53F76D9F9FBD613 CRC64;
                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last amotation update)
Noncapsid protein NS-1 (Nonstructural protein NSI).
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                                                                                                                                                              662 AA
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InterPro; IPR001257; Parvo NSI.
Pfam; PF01057; Parvo NSI; 1.
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                                                                                                                                                          STANDARD;
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P52502;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- FUNCTION: Seems necessary for viral DNA replication.
-1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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Martyn J.C., Davidson B.E., Studdert M.J.;
"Nucleotide sequence of felime panleukopenia virus: comparison with
canine parvovirus identifies host-specific differences.";
J. Gen. Virol. 71:2747-2753(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feline panleukopenia virus (strain 193) (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=10787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1992 (Rel. 21, Created)
1-MAR-1992 (Rel. 21, Last sequence update)
15-DEC-1998 (Rel. 37, Last annocation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
                                                                                                                                                                                                                                                                                                                                                                              75.8%; Score 91; DB 1; Length 392; 65.0%; Pred. No. 7.1e-07; tive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                     Nonstructural protein; Noncapsid protein; DNA replication; ATP-binding.
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                                                                                                                                                                                                                                                                                                            124 131 ATP (POTENTIAL).
392 AA; 43971 MW; B875ADDB4977F616 CRC64;
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EMBL; M36246; AAC37827.1; -.
EMBL; A36608; UYPVFP.
InterPro; IPR0013593; AAA_ATPase.
InterPro; IPR001257; Parvo_NS1.
Pfam; PP01057; Parvo_NS1; I.
SMART; SM00382; AAA; I.
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                                                                                          EMBL; M10824; AAA47160.1; -.
PIR; A03697; UYPVIF.
INTERPIO; IPR0013593; AAA ATPASE.
INTERPIO; IPR001257; PATVO_NSI.
PEAM; PP01057; PATVO_NSI.
SMART; SM00392; AAA; 1.
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nes 13; Conservative
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VNCS_FPV19
ID _VNCS_FPV19
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MEDLINE-91202123; PubMed-2016597;
Kariatsumari T., Horiuchi M., Hama E., Yaguchi K., Ishigurio N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mink enteritis virus (strain Abashiri) (MEV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=10793;
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01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
                                                                                                                                          75.8%; Score 91; DB 1; Length 668; 65.0%; Pred. No. 1.2e-06; iive 4; Mismatches 3; Indels
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407 ATP (POTENTIAL).
23 N -> D (IN REF. 2).
443 I -> V (IN REF. 2).
5755 I -> N (IN REF. 2).
76768 MW; 4F8FEA3EE62D2AE7 CRC64;
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668 AA; 76736 MW; DBD5F9E92113685C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                         668 AA
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(Rel. 12, Last sequence update)
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InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SMART; SM00382; AAA; I.
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                                                                                                                                                           Local Similarity 65.0% tes 13; Conservative
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AC P12929;

DT 01-OCT-1989 (1)
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SIX6 MOUSE STANDARD;
090228; 088423;
28-FEB-2003 (Rel. 41, Created)
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                                                                                                SEQUENCE FROM N.A.
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SIXA HORIVAN
SIXA HORIVAN
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SIXA HUMAN
SIXA OR OPTX2 OR SIXA

"Another Human
SIXA OR OPTX2 OR SIXA
"Another Human
"Another
                                                                                                                                                                                                                                                                        Parrish C.R.;
Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                       MEDLINE=88062992; PubMed=2824850;
Reed A.P., Jones B.V., Miller T.J.;
"Mucleotide sequence and genome organization of canine parvovirus.";
J. Virol. 62:266-276(1988).
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MEDLINE-99310672; PubMed=10381575;
Loez-Rios J., Gallardo M.E., Rodriguez de Cordoba S., Bovolenta P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUBEEye;
Leppert G.S., Yang J.-M., Toy J., Sundin O.H.;
"OFTX2, a novel gene expressed in the eye, belongs to a cluster of sine oculis-related homeobox genes.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                          Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nonstructural protein; Noncapsid protein; DNA replication; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 91; DB 1; Length 668; Pred. No. 1.2e-06; 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DE2CCEA69D2A63A6 CRC64;
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NSI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.26
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M19296; AAA67459.1; --
EMBL; M38245; AAB02798.1; --
EMBL; A22962; UTPVCP.
InterPro; IPR0013593; AAA_ATPA8e.
InterPro; IPR001357; Parvo_NS1.
Pfam; PF01057; Parvo_NS1.
SMART; SM00382; AAA; I.
                                                        Canine parvovirus (strain N) (CPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 SRTCOIFRMHGWNWIKVCHA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRACRIFAFHGWNYVKVCHA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 65.0 es 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  668 AA;
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                              MEDIINE=99443875; PubMed=10512683; Gallardo M.E., Lopez-Rios J., Fernaud-Espinosa I., Granadino B., Sanz R., Ramos C., Ayuso C., Seller M.J., Brunner H.G., Bovolenta P., Rodriguez de Cordoba S.; Genemic cloning and characterization of the human homeobox gene SIX6 reveals a cluster of SIX genes in chromosome 14 and associates SIX6 hemizygosity with bilateral anophthalmia and pituitary anomalies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -I- FUNCTION: May be involved in eye development.
-I- SUBCELLULAR LOCATION: Nuclear (By similarity).
-I- TISSUE SPECIFICITY: Expressed in the developing and adult retina.
Also expressed in the hypothalamic and the pituitary regions.
-I- SIMILARITY: Belongs to the SIX/Sine oculis homeobox family.
-I- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
"Six9 (Optx2), a new member of the six gene family of transcription factors, is expressed at early stages of vertebrate ocular and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Developmental protein; Homeobox; DNA-binding; Nuclear protein.

DNA BIND 128 187

HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.0%; Score 48; DB 1; Length 246; 55.6%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Silver project.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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246 Aa; 27664 MW; 1A5FA3F57A76BC77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0007397; P:histogenesis and organogenesis; TAS. GO; GO:0007601; P:vision; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEAM; PF00046; homeobox; 1.

PRINTS; PR00031; HTHREPRESSR.

PRODOM; PD000010; HOMEOBOX; 1.

SMART; SM00389; HOX; 1.

PROSITE; PS00027; HOMEOBOX 1; FALSE_NEG.

PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH lambrepressr.
InterPro; IPR007105; SIX.
InterPro; IPR007106; SIX_SINE_homeo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-165 FROM N.A.
Kitano T., Kobayakawa H., Saitou N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF031648; AAF04402.1; --
EMBL, AA011785; CAA09773.1; --
EMBL, AF141651; AAD49844.1; --
EMBL, AB041399; BAA94484.1; --
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55 RARAIVAFHGGNYRELYH
                                                                          pituitary development.";
Mech. Dev. 83:155-159(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 61:82-91(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:10892; SIX6.
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Gaps

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Indels

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Q920TG;
28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Polycystic kidney disease and receptor for egg jelly related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0cT-1993 (Rel. 27, Created)
01-0cT-1993 (Rel. 27, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Coat protein (Capsid protein).
Helenium virus S (HelVS).
Viruses; SSRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
MEDLINE=90362082; PubMed=2391504;
Foster G.D., Millar A.W., Meehan B.M., Mills P.R.;
"Nucleotide sequence of the 3'-terminal region of Helenium virus S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the potexviruses coat protein family.
  PROSITE; PSS0071; HOMEOBOX 2; 1.
Developmental protein; Homeobox; DNA-binding; Nuclear protein.
DNA BIND 126 186 HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Gen. Virol. 71:1877-1880(1990).
                                                                                                                                                                                        40.0%; Score 48; DB 1; Length 246; 55.6%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.3%; Score 46; DB 1; Length 299; 43.8%; Pred. No. 5.8;
                                                                              141 141 H -> N (IN REF. 3).
220 220 S -> T (IN REF. 3).
246 AA; 27741 MW; F1332D5E617B2CF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 AA; 32877 MW; ED7E43D54CB20BBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD000603; Pltvir coat; 1.
PROSITE; PS00418; POTEX_CARLAVIRUS_COAT; 1.
                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, D10454; BAA01248.1; -. InterPro. PRO052; Plrvir_coat. Pfam, PF00286; virus P-coat. PRINTS; PR00232; POTXCARLCOAT.
                                                                                                                                                                                                                                                                                                                            || | |||| || :: |
55 RARAIVAFHGGNYRELYH 72
                                                                                                                                                                                                                                                                                            2 RACRIFAFHGWNYVKVCH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ||::| |||: :
187 RVCRLYAPVTWNYMHI 202
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                                                                                                                                                                                                                Local Similarity 55.6
es 10; Conservative
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nes 7; Conservative
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                                                        186
141
220
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                                Developmental | DNA BIND 12 | CONFLICT 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coat protein.
SEQUENCE 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COAT HELVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carlavirus
                                                                                                                                    SEQUENCE
                                                                                                                                                                                        Query Match
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PKDR_MOUSE
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Matches
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Matches
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        STTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.

STRAIN=BALB/c; TISSUE=Embryonic head;
MEDLINE=9910672; PubMed=10381575;
MEDLINE=9910672; PubMed=10381575;
MEDLINE=9910672; Lanew member of the Six gene family of transcription factors, is expressed at early stages of vertebrate ocular and factors, is expressed at early stages of vertebrate ocular and mech. Dev. 83:155-159(1999).

I pituitary development.";
Mech. Dev. 83:155-159(1999).

- - FUNCTION: May be involved in eye development.

- - FUNCTION: May be involved in eye development.

- - TISSUE SPECIFICITY: In the developing embryo, expressed mainly in the ventral optic stalk, optic chiasma, the neural retina and the primordial tissues that give rise to the pituitary/hypothalamus axis. Not expressed in the lens placede.

- - DEVELOPMENTAL STAGE: Expression is first detected in the embryo at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homeobox protein SIX6 (Sine oculis homeobox homolog 6) (Optic homeobox
                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/6;
MEDLINE=98393698; PubMed=9724757;
TOY J., Yang J.-M., Leppert G.S., Sundin O.H.;
The Optx2 homeobox gene is expressed in early precursors of the eye and activates retina-specific genes.";
Proc. Natl. Acad. Sci. U.S.A. 95:10643-10648(1998).
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jean D., Bernier G., Gruss P.;
"Six6 (Optx2) is a novel murine Six3-related homeobox gene that
demarcates the presumptive pituitary/hypothalamic axis and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the SIX/Sine oculis homeobox family. SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF050130; AAC33850.1; -.
EMBL, AF135267; AAD48911.1; -.
EMBL, AA011787; CAA09775.1; -.
EMBL, AK017544; -; NOT_ANNOTATED_CDS.
HSSP; P40424; 1872.
TRANSFAC; T03272; -.
MGD; MG11341840; Six6.
GO; GO:0000543; C:nucleus; ISS.
GO; GO:00005675; F:DNA binding; ISS.
GO; GO:0005515; F:Drotein binding; IPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH lambrepressr.
InterPro; IPR007106; SIX.
InterPro; IPR007106; SIX.
InterPro; IPR007106; SIX.
Pfam; PF00046; homeobox; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99400097; PubMed=10473118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ventral optic stalk.";
Mech. Dev. 84:31-40(1999).
                                                                                                    SIX6 OR SIX9 OR OPTX2. Mus musculus (Mouse).
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                 protein)
                                                                                                                                                                                                                NCBI_TaxID=10090;
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Gaps

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5; Indels

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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     꿃
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                   MEDLINE-99138702; PubMed-9949214;
MEDLINE-99138702; PubMed-9949214;
Hughes J., Ward C.J., Aspinwall R., Butler R., Harris P.C.;
"Identification of a human homologue of the sea urchin receptor for egg jelly: a polycystic kidney disease-like protein.";
Hum. Mol. Genet. 8:543-549(1999).

-!-FUNCTION: May have a central role in fertilization. May generate a Ca(2+) transporting channel directly involved in initiating the acrosome reaction of the sperm.
-!-SUBUNIT: May form homomultimers or heteromultimers in combination with an as yet unidentified subunits.
-!- DEVELOPMENTAL STAGE: Expression begins at about 2 weeks and continues into adult life, mirroring the production of mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLYCYSTIC KIDNEY DISEASE AND RECEPTOR FOR EGG JELLY RELATED PROTEIN.
EXTRACELULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
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Ionic channel; Signal; Glycoprotein; Transmembrane.
SIGNAL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the polycystin family. SIMILARITY: Contains 1 PLAT domain. SIMILARITY: Contains 1 REJ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1338786; Pkdrei.
InterPro; IPR00211; Cat_channel_TrpL.
InterPro; IPR001211; Cat_channel_TrpL.
InterPro; IPR001024; Inpoxygenase LH2.
InterPro; IPR002819; MCAPC,RED-INE.
InterPro; IPR002819; PKD_C,RED-INE.
InterPro; IPR0003915; PKD_C,IPR00110; PKD_C,IPR0003015; PKD_C,IPR001003; PKD_C,IPR001003; PKD_C,IPR00100303; PKD_C,IPR001003; PKD_C,IPR001003; PKD_C,IPR001003; PKD_T,IPR001003; PKD,IPR001003; PKD,I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement ( or send an email to license@isb-sib.ch)
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precursor (PKD and REJ homolog)
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                                                    Mus musculus (Mouse)
                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spermatozoa.
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POTENTIAL.  EXTRACELLULAR (POTENTIAL).  POTENTIAL.  CYTOPLASMIC (POTENTIAL).  REJ.  PLAT.  N-LINKED (GLCNAC) (POTENTIAL).	Score 46; DB 1; Length 2126; ; Pred. No. 39; 2; Mismatches 6; Indels 0; Gaps	20 1997	A8B3 HUMAN STANDARD; PRT; 1310 AA. 060423; Q81048; Q86M22; 30-MAY-2000 (Rel. 39, Creates, Cre	PSEQUENCE FROM N.A. (ISOFORM 2).  TISSUB-EAP, and Testis,  A Kitausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  A Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  A Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  A Brownstein M.J., Wokernan K.J., Malek J.M., Gunble R.H.,  Rachards S., Worley K.C., McKernan K.J., Malek J.M., Gubbs R.A.,  Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  Richards S., Worley K.C., Shevchenko Y., Bouffack G.G.,  A Richards S., Wetteman M., Madan A., Rodrigues S., Sanchez A.  Whiting M., Madan A., Youchman J.W., Green B.D., Dickson M.C.,  Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,  Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,  "Generation and initial analysis of more than 15,000 full-length human and mouse cDAB agenences."
1985 2019 2019 2019 2126 1231 123 1129 1129 1129 1129 1129 1129	38.3%; Similarity 46.7%; 7; Conservative	6 IFAFHGWNYVKVCHA 20 :            :     1983 VFGQHEWNYSNMIHA 19 N	STANDARD; QBNAY8, Q96M22, QBNAY8, Q96M21, 11. 42, Last seque 11. 42, Last anno holipid-transpor- member 3. COR FOS37502_2. RUMan). Zoa, Chordata; C. ria; Primates; C;	(ISOFORM 1)  Peingold 1)  Peingold 1)  Peingold 1)  Peingold 1)  Peingold 1)  Peres N. M.  Pes N. M
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EXTRACELLULAR (POTENTIAL)

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TRANSMEN **TRANSMEN** 

DOMAIN

OMAIN OMAIN

DOMAIN TRANSMEM

**FRANSMEM** 

CYTOPLASMIC (POTENTIAL).

POTENTIAL

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                   Lamerdin J.B., McCready P.M., Skowronski B., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
Robayashi A., Olsen A.S., Carrano A.V.;
Sequence analysis of a 3.5 Mb contig in human 19913.3 containing a
                                                                                                                                                                                             Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawal-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashira H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
                                                                                                                                      serine protease gene cluster.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                     "NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                              Unpublished observations (FEB-2003).
Unpublished observations (FEB-2003).
-!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                          CONCEPTUAL TRANSLATION (ISOFORM 1)
[2]
SEQUENCE OF 173-1310 FROM N.A.
                                                                                                                                                                          SEQUENCE OF 978-1310 FROM N.A.
                                                                                                                                                                                        rissum=Testis,
                                                                                                                                                                                                                                                                                                                                       Axelsen K.
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completed: May 28, 2004, 12:57:42 ne : 7.75 secs Search comp Job time :

collaboration

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or send an email to license@isb-sib.ch)

EMBL; BC033179; AAH33179.1; ALT SEQ. EMBL; AC004755; AAC17601.1; ALT SEQ. EMBL; AK057452; BAB71492.1; ALT INIT

HGNC:13535; ATP8B3

Genew:

605866;

MIM;

EMBL; BC035162; AAH35162.1; -.

InterPro; IPR001757; ATPase\_B1-B2.
InterPro; IPR006539; Flippase.
InterPro; IPR0119; CATATPASE.
TIGRFAMS; TIGR01652; ATPase-Plipid; 1.
PROSITE; PS00119; ATPASE\_B E1 E2; 1.
Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;

POTENTIAL. EXTRACELLULAR (POTENTIAL)

DOMAIN TRANSMEM DOMAIN

RANSMEM *IRANSMEM* 

DOMAIN

CYTOPLASMIC (POTENTIAL)

POTENTIAL. EXTRACELLULAR (POTENTIAL)

Isoīd=060423-2; Sequence=VSP 007304;
-!- SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IV.
-!- CAUTION: Ref.1 (AAH33179) sequence differs from that shown due to presence of unspliced intronic sequence in the C-terminus.
-!- CAUTION: Ref.2 sequence differs from that shown due to erroneous

gene model prediction.

IsoId=060423-1; Sequence=Displayed;
Note=No experimental confirmation available;

Name=2

5 RIFAFHG-WNYVKVC 18 Conservative

1;

Gaps

1;

Score 45.5; DB 1; Length 1310; Pred. No. 29; 4; Mismatches 3; Indels 1.

37.98; 46.78;

Best Local Similarity
Matches 7; Conserv

148029 MW; F1A1C25A8DE696FC CRC64;

1310 AA;

FTIG=VSP

Missing

CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).

(in isoform 2)

POTENTIAL. EXTRACELLULAR (POTENTIAL)

145 151 172 192 217

1146 1152 1173 1193 1218

**RANSMEN** MOD RES

DOMAIN

DOMAIN

949

VARSPLIC SEQUENCE Query Match

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL).

POTENTIAL

1089

TRANSMEM RANSMEM

DOMAIN

Title: Perfect score:

Sequence:

OM protein -

Run on:

Scoring table:

Searched:

Database

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Q84393 canine parv
P89514 feline panl
Q18097 caenorhabdi
Q9v1e6 drosophila
Q9sn6v2 drosophila
Q8sn6v2 drosophila
Q8sn8v6 drosophila
Q8sn2a0 pan troglod
Q9r2a1 pan troglod
Q9r2a9 pongo pygma
Q2r2a3 arabidopsis
Q9ma6 guillardia
Q7mu3 bordetella
Q7wu3 bordetella
Q7wu3 bordetella
Q9v8c drosophila
                                                                                                                                                                                                                                                                          Q8jfz7 xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morgan W.R., Ward D.C.;
"Three splicing patterns are used to excise the small intron common to all minute virus of mice RNAs.";
J. Virol. 60:1170-1174 (1986).
EMBL; J02275; AAA67108.1;
 P89512 feline
P90484 feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MVM(p);
MEDLINE=866115415; PubMed=1502703;
Astell C.R., Gardiner E.M., Tatteraall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice,"
"DNA sequence of the lymphotropic variant of minute virus of mice,"
MVM(1), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M., Ward D.C.; virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                             Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10794;
                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                      721 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MVM(p);
MEDLINE=83143341; PubMed=6298737;
Astell C.R., Thomson M., Merchlinsky
"The complete DNA sequence of minute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parvovirus.";
Nucleic Acids Res. 11:999-1018(1983)
                   Q84393
P89514
Q18097
Q9VLE6
Q9N6V2
Q88W76
                                                                           QBING2
QBIHB6
Q9ZJY7
Q9N2A1
                                                                                                                  Q9N2A0
Q9N299
Q2723
Q9AW86
Q7WP13
Q7W1A9
Q7VUE3
Q9V9Y0
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Q8C0Z9
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MEDLINE=87061199; PubMed=3783817;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prototype strain.";
J. Virol. 57:656-669(1986)
                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                  Nonstructural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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rat parvovi
rat minute
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Q84363 murine minu
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                                                                May 28, 2004, 12:52:08 ; Search time 32 Seconds (without alignments) 197.199 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       feline
feline
feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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Q993m6
Q71159
Q71157
Q81v18
P88899
Q81v28
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P89516
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P89513
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       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                        1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                              protein search, using sw model
                                                                                                                        TRACRIFAFHGWNYVKVCHA 20
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Q993M6
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Q8JV28
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P89515
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P89513
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_phage:*
sp_plant:*
sp_rodent:*
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sp_bacteriap:*
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sp_bacteria:*
sp_fungi:*
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Rat parvovirus type 1: the prototype for a new rodent parvovirus
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MEDLINE=21102993; PubMed=11172095;
Ball-Goodrich L.J., Johnson E., Jacoby R.;
"Divergent replication kinetics of two phenotypically different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                                       Autonomous rat parvovirus RV-Y.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=155025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=U-Mass;
MEDLINE=99184569; PubMed=9525656;
Ball-Goodrich L.J., Leland S.E., Johnson E.A., Paturzo F.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 397;
                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 AA; 43959 MW; D62052E4767366BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    665 AA; 75375 MW; 778E29043417E409 CRC64;
672 AA; 76112 MW; 31C6365276727363 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Nonstructural protein 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.3%; Score 106; DB 12;
85.0%; Pred. No. 4.4e-08;
iive 1; Mismatches 2;
                                   93.3%; Score 112; DB 12;
85.0%; Pred. No. 9e-09;
sive 2; Mismatches 1;
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EMBL; AF317513; AAK27438.1; -
InterPro; IPR001257; Parvo NS1.
Pram; PF01057; Parvo NS1; J.
NOW TER
SEQUENCE 397 AA; 43959 MW; D620
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                                                                                                           1 TRACRIFAFHGWNYVKVCHA 20
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J. Virol. 72:3289-3299(1998).
EMBL; AF036711; AAC40695.1; -.
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
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Best Local Similarity 85.0
Matches 17; Conservative
                                   Query Match
Best Local Similarity 85.0
Matches 17; Conservative
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Kilham rat virus.
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Ball-Goodrich L.J., Johnson E.;
"Molecular characterization of a newly recognized mouse parvovirus.";
J. Virol. 68:6476-6486(1994).
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MEDLINE=66115415; PubMed=3502703;
MEDLINE=66115415; PubMed=3502703;
MEDLINE=66115415; PubMed=1502703;
"DNA sequence of the lymphotropic variant of minute virus of mice,
MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                  NS1.
Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10794;
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NCBI_TaxID=35340;
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Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U12469; AAR61405.1; ...
InterPro; IFR01257; Parvo NS1.
Pfam; PF01057; Parvo NS1.
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prototype strain.";

J. Virol. 570:656-669(1986).
EMBL; M12032, AAA6556.1; -.
PIR; A23008; UYPVIM.
InterPro; IPRO01257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SEQUENCE 721 AA; 81863 MW; 9FD29C327C7F4BBF CRC64;
   Pfam; PF01057; Parvo NS1; 1.
SEQUENCE 721 AA; 91896 MW; 18391758E42F0DCF CRC64;
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Last annotation update)
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94.2%; Score 113; DB 12;
Best Local Similarity 90.0%; Pred. No. 6.8e-09;
Matches 18; Conservative 1; Mismatches 1;
                                                         96.7%; Score 116; DB 12;
95.0%; Pred. No. 2.4e-09;
live 0; Mismatches 1;
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                           Local Similarity 95.0
nes 19; Conservative
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NS1.
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01-JUN-2003
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RESULT 3
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Indels

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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI TaxID=12441;
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85.0%; Pred. No. 7.4e-08;
tive 1; Mismatches 2; Indels (
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Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
                                                                                                                                                                                                                                                                                                                                                                                 "Sequence of a Diabetogenic Parvovirus of Rats.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U79033; AAB38326.1; -.
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1.
SEQUENCE 672 AA; 76056 MW; 0299B36871A0A10A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         parvoviruses.";
J. Gen. Virol. 83:2075-2083(2002).
EMBL; A321230; AAM93272.1; -.
InterPro; IPRO157; Parvo NS1.
Pfam; PF01057; Parvo N31; I.
SEQUENCE 672 AA; 75987 MW; 22B4611C20CDB6E9 CRC64;
                                                                                                                                                              Last sequence update)
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01-OCT-2002 (TrEMBLrel. 22, Created)
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361 TRICRIFAEHGWNYIKVCHA 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 85.01
Matches 17; Conservative
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Brown D.W., Like A.A.;
                                                                                                                                                                                                      Non-capsid protein
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QBJV14
ID QBJV1,
AC QBJV1,
DT 01-OC
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Q8JV28
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                                                                                                                                                                                                                                                                                                                                                Rat parvovirus la.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=74581;
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88.3%; Score 106; DB 12; Length 672;
Best Local Similarity 85.0%; Pred. No. 7.4e-08;
Matches 17; Conservative 1; Mismatches 2; Indels 0;
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Viruses; 88DNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=172385;
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85.0%; Pred. No. 7.4e-08;
ive 1; Mismatches 2; Indels
88.3%; Score 106; DB 12; Length 665; 85.0%; Pred. No. 7.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=99184569; PubMed=9525656;
Ball-Goodrich L.J., Leland S.E., Johnson E.A., Paturzo F.X.,
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BEDLINE=22120170; PubMed=12124471; Mar C.H., Soderlund. M., Pintel D.J., Riley L.K.; Man C.H., Soderlund characterization of three newly recognized rat
                                       2; Indels
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J. Gen. Virol. 83:2075-2083(2002).
EMBL; AF332882; AAM93275.1; -
InterPro. I FR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; 1.
SEQUENCE 672 AA; 76059 MW; 63D8B9EBF99E07B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serogroup.";
J. Virol. 72:3289-3299(1998).
BEMBL, AR036710; AAC40693.1; -.
InterPro; IRR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; 1.
SEQUENCE 671 AA; 75752 MW; 9BCB39A39298D4DE CRC64;
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Last annotation update)
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Last sequence update)
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                                       1; Mismatches
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                                                                                                    354 TRTCRIFAEHGWNYIKVCHA 373
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                                                                               1 TRACRIFAFHGWNYVKVCHA 20
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                                       17; Conservative
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Best Local Similarity
Matches 17; Conserv
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RESULT 7 Q8JV18

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'Evolutionary pattern of feline panleukopenia virus differs from that
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nonstructural protein 1.
Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBL_TaxID=10786;
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Local Similarity 65.0%; Pred. No. 1.4e-05;
Les 13; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                        3; Indels
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                                                                          canine parvovirus.";
submitted (DEC-1996) to the EWBL/GenBank/DDBJ databases
EMBL, ARD000065; PAA19023.1;
GO; GO; 0000166; F:nuclectide binding; IEA.
InterPro; IPR001257; PATVO NS1.
InterPro; IPR001257; PATVO NS1.
Pfam; PF01057; PATVO NS1.
SMART; SM00382; AAA, 1.
SEQUENCE 668 AA; 76755 MW; 37ABDFD347017F52 CRC64;
                                                                                             to the EMBL/GenBank/DDBJ databases
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InterPro; IPR001553; AAA ATPase.
InterPro; IPR001257; Parvo NSI.
Pfam; PF01057; Parvo NSI; I.
SEQUENCE 668 AA; 1.
SEQUENCE 668 AA; 76741 MW; 2413B450EC9161BD CRC64;
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Feline panleukopenia virus (FPV)
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nes 13; Conservative
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STRAIN=TUB;
Horiuchi M.;
FROM N.A.
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NCBL_TaxID=10786;
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                                     Horiuchi M.;
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P90449
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                                                                  Rat minute virus 1c.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=172387;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=172386;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10786;
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                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-22120170; MEDLINE-22120170; PubMed-12124471; WAN C.H., Soluthor Characterization of three newly recognized rat
                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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J. Gen. Virol. 83:2075-2083 (2002).

EMBL; AR332883; AAM93277.1; -.

EMBL; PR332083; Parvo NS1.

Pfam; PF01057; Parvo NS1; I.

SEQUENCE 672 AA; 76201 MW; C2F1A71F6EF449A6 CRC64;
                                                                                                                                                                                                                                             parvoviruses.";
J. Gen. Virol. 83:2075-2083(2002).
EMBL; AF312884; AAM93279.1; -.
InterPro; IPRO01257; Parvo NS1.
SEQUENCE 672 AA; 75988 MW; 52DF6549349CF3FD CRC64;
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Nonstructural protein 1.
Feline
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Last sequence update)
Last annotation update)
  01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  Score 106; DB 12;
Pred. No. 7.4e-08;
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88.3%; Score 106; DB 12;
Best Local Similarity 85.0%; Pred. No. 7.4e-08;
Matches 17; Conservative 1; Mismatches 2;
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Best Local Similarity 85...
Local 17; Conservative
                                         Nonstructural protein 1.
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01-MAY-1997 01-MAY-1997

RESULT 12
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AC P8951
DT 01-MA
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Nonstructural protein 1.
Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

REBL; AB000069; BAA19030.1; ---

EMBL; AB000063; BAA19034.1; ---

GO; GO:0019012; C:virion; IEA.

GO; GO:000166; F:nucleotide binding; IEA.

RINterPro; IPR001357; AAA_ATPase.

RINterPro; IPR001357; Parvo NS1.

R SMART; SMO0382; AAA; 1.

R SMART; SMO0382; AAA; 1.

R NOMETUCURAL PROCEGIN.

SEQUENCE 668 AA; 76769 MW; OECAFEGBF62A5DE0 CRC64;
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Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
Resul, AB000065; BAA19028.1; -..
EMBL, AB000065; BAA19026.1; -..
EMBL, AB000065; GaA19026.1; -..
RO; GO:0019012; Civirion; IEA.
RO; GO:001066; F:nuclectide binding; IEA.
RICEPRO; IPR001357; AAA ATPase.
R InterPro; IPR001357; Parvo_NS1.
R Pfam; PP01057; Parvo_NS1.
R SMART; SM00382; AAA; 1.
R Nonstructural protein.
SEQUENCE 668 AA; 76755 MW; 008CED50178833EF CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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1 TRACRIFAFHGWNYVKVCHA 20

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Sequence 4915, Ap
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Sequence 5612, Ap
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                            OM protein
                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                   Perfect
                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
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Sequence 5949, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                         18934, A
7, Appli
7, Appli
7, Appli
133027, A
                                 3, Appli
1, Appli
2, Appli
4, Appli
19224, A
2, Appli
2, Appli
2, Appli
                                                                                                                                                                                                                                                                          Sequence 33027, A
Sequence 22448, A
Sequence 12, Appl
              Sequence
Sequence
Sequence
Sequence
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Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                    US-09-004-393B-2
US-09-004-393B-4
US-09-252-991A-19224
US-08-964-127-2
US-10-000-273-2
US-09-348-006B-7
US-08-348-006B-7
US-08-348-006B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTKY: CO.,

ZIP: 0.2354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
PLING DATE: 30-Jun-1998
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 July 2, 1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 60/489
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION POPE SEQ 1D NO: 5949:
SEQUENCE CHARACTERISTICS:
TENGTH: 79 amino acid8
                                                                                                                                                                                                                                                                      US-09-252-991A-33027
US-09-252-991A-22448
US-08-948-569A-12
              PCT-US93-08528-47
                                   US-07-629-104I-3
                                                     JS-08-288-663A-1
                                                                                                                                                                                                                                                       JS-09-158-657-7
                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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197 RVCRLYAPLTWNYM 210
                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Hop latent viroid
                                                                                                                                                                                                                                                                                                                                                                                                                              2 RACRIFAFHGWNYV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                           Sequence 6, Application US/08736723A
; Sequence 6, Application US/08736723A
; Patent No. 5869235
; GENERAL INFORMATION:
; APPLICANT: SUDA, NARUSHI
APPLICANT: TIOGA, YUTARA
; TITLE OF INVENTION: GENE OF THE HOP LATENT VIRUS AND METHODS
; TITLE OF INVENTION: POR DETECTING THE SAME
NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFPERSON DAVIS HIGHWAY, SUITE 400
CITY: ALINGTON
                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 2; Length 306;
Pred. No. 32;
3; Mismatches 4; Indels
Length 79;
                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-UCS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/736,723A
FILING DATE: 25-OCT-1996
CLASS/FICATION DATA:
APPLICATION NUMBER: UP 7-302297
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 7-352285
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: UP 7-352285
FILING DATE: 28-DEC-1995
ATCHNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2589-042-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 6, Application US/09221114A; Patent No. 6132960; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.7%;
  Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ||::| |||:
197 RVCRLYAPLTWNYM 210
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                                                                                                                         19 KMČŘLFIYHGKŇVV 32
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Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                    RESULT 2
US-08-736-723A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-736-723A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-221-114-6
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Sequence 11397, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: PUEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
ENGINE 203

LENGTH: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQUERAL INFORMATION:
Patent No. 6610836
GENERAL INFORMATION:
PAPPLICANT GALY Breton et. al
APPLICANTION:
APPLICANTION:
TITLE OF INVENTION:
PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 2000-01-29
RIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 14279
LENGTH: 388
LENGTH: 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
APPLICANT: HATAYA, TASSUZI
TITLE OF INVENTION: GENE OF THE HOP LATENT VIRUS AND METHODS FOR DETECTING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 2580-0068-0D1V
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 08/736,723
EARLIER APPLICATION NUMBER: 08/736,723
EARLIER APPLICATION NUMBER: 09/736,723
EARLIER FILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENT VET: 2.1
SOFTWARE: PATENT VET: 2.1
SOFTWARE: PATENT VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.7%; Score 44; DB 4; Length 388; 100.0%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 3; Length 306;
Pred. No. 32;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 36.7%; Score 44; Best Local Similarity 50.0%; Pred. No. Matches 7; Conservative 3; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14279
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
NUMBER OF SEQ ID NOS: 8252
LENGTH: 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: HAMILTON, BROOK, SMITH & REYNOLDS, P.C. Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBSTRATE TRAPPING PROTEIN TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE: 25-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION 0435
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 4
Pred. No. 40;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 2
Pred. No. 49;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/08685992
Patent No. 5912138
                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Acinetobacter baumannii
US-09-328-352-5612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 ACDVVDMEGYALAKVCH 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ACRIFAFHGWNYVKVCH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE
TITLE OF INVENTION: TYROSINE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.0%;
Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Window
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 232 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 781-861-9540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
         6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-685-992-27
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Patent No. 6605709
GENERAL INPORMATION:
APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
TITLE OF INVENTION: US/09/543,681A
FILE REFERENCE: 2709.1002-001
FILE REFERENCE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5660
LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4915, Application US/09543681A
Sequence 4915, Application US/09543681A
Sequence 4915, Application US/09543681A
Sequence 4915, Application US/09543681A
Sequence 4915, Application US/09543681A
Sequence 4915, Application US/09543681A
Sequence 4915, Application US/09543681A
Sequence 4915, Application US/09543681A
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                                                                                          Query Match 35.8%; Score 43; DB 4; Length 203; Best Local Similarity 39.1%; Pred. No. 30; Matches 9; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 897;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 4;
Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                2 RACRIFAFHGW----NYVKVCHA 20
                                                                                                                                                                                                                                               63 RACRMSSPTGWYLLQALISACHA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5612, Application US/09328352
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70 ACQLGIMYLFVFHAYNYLTV 89
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.8%;
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Similarity 40.0%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||| ||| :||
292 IFAGAGWNVIKV 303
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Best Local Similarity
Matches 8; Conserva
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US-09-328-352-5612
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1155 AVENUE OF THE AMERICAS
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/015,985
FILING DATE: 10-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-020
                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 233 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 SRQIRQFHFHGWPEVGI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TRACRIFAFHGWNYVKV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS: single
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                        STATE: NEW YORK COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-015-985-11
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APPLICANT: Schlessinger, Joseph
APPLICANT: Sap, Jan M.
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-ALPHA
                                                                                                                                                                 Sequence 27, Application US/09144925
Patent No. 5951979
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Tonks, Andrew J.
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/685,992
FILING DATE: July 25,1996
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFANK: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/08015985 Patent No. 5538886
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 SRQIRQFHFHGWPEVGI 191
                                                                 175 SROIROFHFHGWPEVGI 191
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                           1 TRACRIFAFHGWNYVKV 17
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SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-09-144-925-27
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US-09-144-925-27
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Sequence 11, Application US/09280597

Patent No. 6682905

GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-ALPHA
NUMBER OF SEQUENCE: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: NEW YORK
STREET: NEW YORK
STREET: 10036
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER: IBM PC compatible
COMPUTER: DEFAITING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
SOFTWARE TO STATEM TO STATEM TO SOFTWARE THING NUMBER: US/08/015,985
FILING DATE: US-0FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGRYT INFORMATION:
NAME: COTUZZI, LAURA A. REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-020
TELEPRANIS (212) 790-9090
TELEPRAN: (212) 790-9090
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,597
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Pred. No. 1.6e+02;
2; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: Sap, Jan M.
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-ALPHA
NUMBER OF SECTIONCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,597
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STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
COUNTRY: U.S.*
FILING DATE: 10-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LBULTA A.
REGISTRATION NUMBER: 30,742
RERENENCE/DOCKET NUMBER: 7683-020
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEXA: (212) 869-9741/8864
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.0%; Score 42;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/015,985
FILING DATE: 10-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 7683-TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 969-9090 TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09280597
Patent No. 6682905
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677 SRQIRQFHFHGWPEVGI 693
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Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                    : 793 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 793 amino acids TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                        US-08-015-985-3
                                                                                                                                                                                                                                                                      LENGTH:
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Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 2709-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
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; Patent No. 5538886
; GENERAL INPORMATION:
    APPLICANT: Schlessinger, Joseph
    APPLICANT: Schlessinger, Joseph
    TITLE OF INVENTION: PHOSPHATASE-ALPHA
    ITLE OF INVENTION: PHOSPHATASE-ALPHA
    NUMBER OF SEQUENCE: 14
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: PENNIE & EDMONDS
    STREET: 1155 AVENUE OF THE AMERICAS
    CITT: NEW YORK
                                                                                                                                                                                                                                                                                        Score 42; DB 4; Length 233;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 323;
68;
                                                                                                                                                                                                                                                                                                                                  7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.0%; Score 42; DB
35.7%; Pred. No. 68;
tive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                    TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: MOLECULE TYPE: protein
US-09-280-597-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
        FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    129 SRQIRQFHFHGWPEVGI 145
                                                                                                                                                                                                                                                                                                                                                                            1 TRACRIFAFHGWNYVKV 17
                                                                                                                                                                                                                                                                                      Query Match 35.0%;
Best Local Similarity 47.1%;
Matches 8; Conservative
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90 CVVYCVAGWSFIKV 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 35.0
Best Local Similarity 35.7
Matches 5; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: M.catarrhalis
US-09-540-236-2794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: NEW YORK COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-540-236-2794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2794
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-08-015-985-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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0; Gaps Best Local Similarity 47.1%; Pred. No. 1.6e+02; Matches 8; Conservative 2; Mismatches 7; Indels

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Search completed: May 28, 2004, 13:02:03 Job time : 13.5 secs

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44
16
                                                                                                                                                                                                                                                                                                                                              May 28, 2004, 12:57:09; Search time 34.75 Seconds (without alignments)
160.719 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Cgn2_6/ptodata1/pubpaa/US07_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US06_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/pubpaa/PCUS_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US08_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US08_NEW_PUB.pp:*
| Cgn2_6/ptodata1/pubpaa/US09_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US09_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US09_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US10A_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US10A_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US10A_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US10_NEW_PUB.ppp:*
| CGn2_6/ptodata1/pubpaB.ppp:*
| CGn2_6/ptodata1/pubpaa/US10_NEW_PUB.ppp:*
| CGn2_6/ptodata1/pubpaa/US10_NEW_PUB.ppp:*
| CGN2_6/ptodata1/pubpaa/US10_NEW
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                                                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1151071 segs, 279249464 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications AA:*
                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Maximum DB E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
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Description 2 US-10-335-977-6003 2 US-10-235-977-6004 2 US-10-235-977-6004 2 US-09-764-869-901 4 US-10-091-504-901 5 US-10-277-577-901 5 US-10-277-577-901 5 US-10-277-577-901 5 US-10-276-579-149096 US-09-764-877-1359 5 US-10-42-515-1359 5 US-10-42-515-1359 6 US-10-242-515-1359 7 US-10-249-484 6 US-10-259-144-24 7 US-10-259-144-24 7 US-10-276-774-2484 SUMMARIES Query Match Length DB 48 48 47.5 47 4 C A 4 4 4 4 4 4 4 4 4 C N 4 4 4 4 4 4 4 4 4 Score Result Š

Sequence 19, Appl Sequence 54, Appl Sequence 1249, App Sequence 1249, App Sequence 1139, Appl Sequence 10, Appl Sequence 1159, App Sequence 1159, A Sequence 1151, A Sequence 1151, A Sequence 16117, A Sequence 12217, A Sequence 12217, A Sequence 20777, A Sequence 20777, A Sequence 20777, A Sequence 20177, A Sequence 20177, A Sequence 2110, Appl Sequence 2110, Appl Sequence 4, Appl Sequence 4, Appl Sequence 2110, Appl Sequence 21587, Sequence 215887, Sequence 10481, A Sequence 6584, A	EQUENCES RI FOR
14 US-10-163-866-39 15 US-10-163-866-54 15 US-10-295-027-1249 16 US-10-295-027-1249 17 US-10-295-027-1249 18 US-10-214-8678-10 18 US-10-214-8678-10 19 US-10-425-114-63759 12 US-10-425-114-63759 12 US-10-425-114-63759 13 US-10-282-1138-65198 14 US-10-283-128-65198 15 US-10-283-128-65198 16 US-10-425-138-63215 17 US-10-424-59-186241 18 US-10-156-761-12277 19 US-10-156-761-12277 19 US-10-156-761-12677 10 US-09-964-259-4 10 US-09-964-259-4 11 US-10-156-761-8366 12 US-10-424-599-203396 13 US-09-964-259-4 14 US-10-156-761-8366 15 US-10-424-599-215587 15 US-10-188-832-70 17 US-09-864-761-46384 18 US-10-164-8848-10481 18 US-10-164-8848-10481 18 US-10-166-6384	ALIGNMENTS  7-6003  001, Application US/1035977  10. US20040052799A1  INFORMATION: LICANT: DOUGLAS SMITH et al LECANT: DOUGLAS SMITH et al LECANTION: NUCLEIC ACID AND AMINO ACID SEQUENCES BERRATICA ADDRESS: 10031  SERCATICA ADDRESS: 10031  STATE: MASSACHUSE & COCKFIELD STATE: MASSACHUSE & COCKFIELD STATE: MASSACHUSE & STEECT CITY: BOSTON STATE: MASSACHUSE & COCKFIELD STATE: MASSACHUSE & COCMPATION MEDIUM TYBE: CD/ROM: MARE: MANDARE: OS/93,002  FILING DATE: 17-DEC-1997  ONE STATE: MASSACHUSE: ANY E. REGISTRATION NUMBER: 36,207  TELEPRAX: (617)227-7400
507 14 507 15 507 16 507 17 50	15-977-6003  Ice 6003, Application US/103359  Ication No. USZO040052799A1  RAPLICANT: DOUGLAS SMITH et a  TITLE OF INVENTION:  RELATING  DIAGNOSTI  NUMBER OF SEQUENCES: 10031  CORRESPONDENCE ADDRESS:  ADDRESSE: LAHIVE & COCKI STREET: 28 State Street  CITY: Boston STREET: 28 State Street  CONNTRY: USA  ZIP: 02109-1875  COMPUTER: IBM PC Compatil OPERATING SYSTEM: Window SOFTWARE: UNIX CURRENT APPLICATION DATA:  APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: RILNG DATE: 17-DEC-197  ATTORNEY/AGENT INFORMATION: NAME: MANDERS: 36, REGISTRATION NUMBER: 36, TELERPHONE: (617)227-7400  TELERPHONE: (617)227-7400  TELERPHONE: (617)227-7400  SEQUENCE CHARACTERISTICS: LENGTH: 69 amino acids
	-977-6003 e 6003, Application AL INFORMATION: APPLICANT: DOUGLAS; TITLE OF INVENTION: ADDRESSES: LAH; ADDRESSES: LAH; ADDRESSES: LAH; STREET: 28 StatCITY: BOSTON ADDRESSES: LAH; COMPUTEY: USA ZITE: MASSEACH COMPUTER: EDMINATION: MEDIUM TYPE: COMPUTER: EDMINATION IN PELICATION NU FILING DATE: 1 ATTORNEY, APPLICATION IN FILING DATE: 1 ATTORNEY, AGENT INFO NAME: MANDE: ATTORNEY, AND APPLICATION NU FILING DATE: 1 ATTORNEY, AGENT INFO NAME: MANDE: G17) ATTORNEY, AGENT INFO NAME: MANDE: G17) MATTON FOR SEQ ID NI SEQUENCE CHARACTERI LENGTH: 69 ami:
<b>຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺຺</b>	6003 3, Applic. Mo. US200 OF INVENTED DOUGE INVENTED DOUGE INVENTED DOUGE SEGUIT DOUGE SEGUIT DOUGE SEGUIT DOUGE SEGUIT DOUGE SEGUIT DOUGE SEGUIT TO SEGUIT TO SEGUIT TO SEGUIT TO SEGUIT DOUGE SEGUIT SEGUIT DOUGE SEGUIT DOUGE SEGUIT SEGUIT DOUGE SEGUIT SEGUIT DOUGE SEGUIT SEGUIT DOUGE SEGUIT SEGUI
4 4 4 4 4 4 4 4 4 በ ነርርርርርርርርርርርርርርርርርርር	LT 1  Consider the construction of the constru
11111000000000000000000000000000000000	RESULT 1  US-10-335-977-6003 Sequence 6003, Application US Publication No. US20040052799 GENERAL INFORMATION: APPLICANT: DOUGLAS SMI TITLE OF INVENTION: NU TITLE OF INVENTION: NU TITLE OF INVENTION: NU STREET: 28 State COUNTRY: BOSTON STRATE: MASSACHUSE COUNTRY: USA ZIP: 02109-1875 COMPUTER READABLE FORM MEDIUM TYPE: CD/R COMPUTER: IBM PC OPERATION TYPE: CD/R COMPUTER: 1BM PC OPERATION TYPE: CD/R COMPUTER: 1BM PC OPERATION TYPE: USA SOFTWARE: UNIX CURRENT APPLICATION DATA APPLICATION NUMBE FILING DATE: 17-D ATTORNEY/AGENT INFORMA NAME: MANDE: MANDE: NUMB REFREENCE/DOCKET TELECOMMUNICATION INFO TELECOMMUNICATION I

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us-10-069-056-9.rapb

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TITLE OF INVENTION: Identification of Bssential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 50921
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 323;
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, APPLICANT: Rosen et al.
, TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
Indels
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Pred. No. 59;
3; Mismatches 4;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                | |::|:||:
95 CLIWSFNGWSFWEVTGLFLFYVVVCSA 121
                                              4 CRIFAFHGWN-----YVKVCHA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-28
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2001-02-09
                                                                                                                                                                                                           Sequence 50921, Application US/10282122A Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bordetella pertussis
US-10-282-122A-50921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.6%;
36.4%;
                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto, Robert
Forsyth, R.
Xu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 RIFAFHGWNYVKV----
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Best Local Similarity 36.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Zyskind, Judith
Wall, Daniel
    10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trawick, John
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-09-764-869-901
       Matches
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Sequence 6004, Application US/10335977
Sequence 6004, VB20040052799A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 12; Length 136;
Pred. No. 22;
                                                                                                                                                                                                                                                                                       Score 48; DB 12; Length 69;
Pred. No. 12;
4; Mismatches. 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC COMPACTION
SOFTWARE: UNIX
CURRENT APPLICATION DATE:
RILING DATE: 30-Dec-2002
PRIOR APPLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-197
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELECHMONIS: (6.7)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...136
SEQUENCE DESCRIPTION: SEQ ID NO: 6004:
                                                                                                                                                 ), NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...69
; SEQUENCE DESCRIPTION: SEQ ID NO: 6003:
US-10-335-977-6003
                                                                                                                                                                                                                                                                                                                                                                                          4 CRIFAFHGWN-----YVKVCHA 20
                                                                                                                                                                                                                                                                                                                                                                                                                       CLIWSFNGWSFWEVTGLFLFYVVVCSA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Helicobacter pylori
              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 6004
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 10031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.0%;
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 37.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE
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Best Local Similarity
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Gaps

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**Gaps** 

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Sequence 149096, Application US/10424599

Sequence 149096, Application US/10424599

Publication No. US/20040031072A1

Publication No. US/20040031072A1

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cav Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE OF INVENTION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 149096

LENGTH: 187
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-11
PRIOR PILING DATE: 2000-07-11
PRIOR PILING DATE: 2000-08-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 901
LENGTH: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1359, Application US/09764877

Patent No. US20020147140A1

GENERAL INFORMATION:

ADFLICANT: Rosen et al.

TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC005

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1359

LENGTH: 50
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                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 15; Length 54;
Pred. No. 13;
3; Mismatches 2; Indel8
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_105657C.1.pep
US-10-424-599-149096
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Pred. No. 69;
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Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRACRIFAFHGWNYV 15
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Best Local Similarity 80.0
Matches 8; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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US-10-424-599-149096
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Sequence 901, Application US/10227577

Publication No. US2004000557541

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007C2

CURRENT APPLICATION NUMBER: US/10/227,577

CURRENT FILING DATE: 2002-08-26

PRIOR APPLICATION NUMBER: 10/091,504

PRIOR APPLICATION NUMBER: 09/764,869

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2000-01-31

PRIOR PLIING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31
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Publication No. US20030059908A1

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC007C1

CURRENT APPLICATION NUMBER: US/10/091,504

CURRENT FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 2442

Prior Application removed - See File Wrapper or Palm

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 901

LENGTH: 54
                              CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 901
LENGTH: 54
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                                                                                                                                                                                                                                                                                     Query Match 39.2%; Score 47; DB 9; Length 54; Best Local Similarity 53.3%; Pred. No. 13; Matches 8; Conservative 3; Mismatches 2: Timfale
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TSACO--SYHSWNYV 21
                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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       FILE REFERENCE: PC007
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Best Local Similarity
Matches 8; Conserv
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US-10-091-504-901
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US-10-227-577-901
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us-10-069-056-9.rapb

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APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Gldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Rarry S.
APPLICANT: Goldman, Rarry S.
APPLICANT: Goldman, Marry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: 2003-02-28
CURRENT FILING DATE: 2003-02-28
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Pred. No. 98;
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                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: PAT_MRT3847_115116C.1.pep
                                                                                                                                                                                                                                                                                                                  Score 44; DB 12;
Pred. No. 98;
2; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 23087
LENGTH: 421
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Publication No. US20030233675A1
GENERAL INFORMATION:
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55.6%;
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Best Local Similarity 38.5%;
Matches 5; Conservative
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 159576
LENGTH: 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-238-075-911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 FAFHGWNYVKVCH 19
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 HGWNYVKVC 18
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                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                   US-10-424-599-159576
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Canou                                                                                                                                                 ö
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC005C.

CURRENT APPLICATION NUMBER: US/10/242,515

CURRENT FILING DATE: 2000-09-13

FRIOR PELING DATE: 2000-01-11

FRIOR APPLICATION NUMBER: 60/180,628

FRIOR APPLICATION NUMBER: 60/180,628

FRIOR APPLICATION NUMBER: 60/214,886

FRIOR PILING DATE: 2000-05-04

FRIOR PILING DATE: 2000-05-18

FRIOR PELING DATE: 2000-05-18

FRIOR APPLICATION NUMBER: 60/217,487

FRIOR APPLICATION NUMBER: 60/225,758

FRIOR APPLICATION NUMBER: 60/225,758

FRIOR PILING DATE: 2000-07-11

FRIOR APPLICATION NUMBER: 60/225,447

FRIOR APPLICATION NUMBER: 60/218,290

FRIOR FILING DATE: 2000-07-14

FRIOR APPLICATION NUMBER: 60/218,290

FRIOR FILING DATE: 2000-07-14

FRIOR APPLICATION NUMBER: 60/216,218,290

FRIOR FILING DATE: 2000-07-14

FRIOR APPLICATION NUMBER: 60/218,290

FRIOR FILING DATE: 2000-07-14

FRIOR APPLICATION NUMBER: 60/218,290

FRIOR FILING DATE: 2000-07-14

FRIOR FILING DATE: 2000-07-14

FRIOR FILING DATE: 2000-07-14

FRIOR APPLICATION NUMBER: 60/218,290

FRIOR FILING DATE: 2000-07-14

FRIOR FILING DATE: 2000-07-14

FRIOR FILING DATE: 2000-07-14

FRIOR APPLICATION NUMBER: 60/218,290

FRIOR FILING DATE: 2000-07-14
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Pred. No. 33;
                                                                         DB 9; Length 50;
                                                                      Score 44; DB 9
Pred. No. 33;
3; Mismatches
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                                                                  36.7%;
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SEQ ID NO 1359
LENGTH: 50
                                                                      Query Match 36.7
Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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US-10-242-515-1359
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US-10-424-599-159576
US-09-764-877-1359
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US-10-163-866-38
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Sequence 2484, Application US/10276774

Sequence 2484, Application US/10276774

Publication No. US20040053245A1

GENERAL INFORMATION:

APPLICANT: Hyeeq, Inc.

APPLICANT: Hyeeq, Inc.

TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides

TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides

CURRENT PLICATION NUMBER: US/10/276,774

CURRENT PILING DATE: 2002-11-18

CURRENT PILING DATE: 2002-11-18

PRIOR FILING DATE: 2000-04-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Zhu, Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
                                                Gaps
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100.0%; Pred. No. 2.5e+02;
Live 0; Mismatches 0; Indele
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LCCATION: (118).
COTHEN INFORMATION: Xaa = any naturally occuring amino acid
US-10-259-194A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TILE OF INVENTION OF TRANSPORTED AND CHARACTERIZATION OF THE REPERENCE 70029-NP CURRENT APPLICATION NUMBER: US/10/259,194A CURRENT APPLICATION NUMBER: US/01/25,277 PRIOR PELING DATE: 2001-09-26 PRIOR PELING DATE: 2001-09-26 PRIOR PELING DATE: 2002-04-04 PRIOR PELING DATE: 2002-04-04 PRIOR PLING DATE: 2002-04-04 PRIOR APPLICATION NUMBER: US/0370,620 PRIOR PLING DATE: 2002-04-04 PRIOR PRIOR DATE: 2002-04-04 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR DATE: 2002-04-04 PRIOR P
Best Local Similarity 38.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 5; Mismatches 3; Indels
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; Sequence 24, Application US/10259194A
; Publication No. US20040010815A1
; GENERAL INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lange, Markus B.
APPLICANT: Ghassemian, Majid
APPLICANT: Briggs, Steven P.
APPLICANT: Gooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Katagiri, Fumiyaki
Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moughamer, Todd
Provart, Nicholas
Ricke, Darrell
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239 CKLYGFSLWNYLR 251
                                                                                                                           4 CRIFAFHGWNYVK 16
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                                                                                                                     36.7%; Score 44; DB 12; Length 507; 60.0%; Pred. No. 2.9e+02; tive 3; Mismatches 1; Indels
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PRIOR FILING DATE: 2000-02-03
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SOFTWARE: CUSTOM
SEQ ID NO 2484
LENGTH: 507
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Matches 6; Conservative
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251 LFAYGGWNYL 260
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                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-10-276-774-2484
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US-10-163-866-38
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Best Local Similarity
Matches 6; Conserv
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June 2, 2004, 15:24:48; Search time 652 Seconds (without alignments) 3988.623 Million cell updates/sec
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GenCore version 5.1.6
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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PAT 30-MAY-2001

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FEATURES

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TQNTGEAGSKACQDGGLSPTWSEIBEDLRACFGAREPLKKDFSBFLNLD"
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Parvovirus ns1 variants
Patrot: EP 1077260-A 4 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts (DE)
1141 ATTTGCTGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGACCA 1200
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Patent: EP 1077260-A 1 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
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Sequence 1 from Patent EP1077260.
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AX137736.1 GI:14273909
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AX137739
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Parvovirus ns1 variants
Patent: EP 1077260-A 12 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
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DEFINITION

AX137747 LOCUS

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ACCESSION VERSION

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

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PAT 30-MAY-2001

Best Loca Matches

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Query Match
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PAMVM2
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TYPPROGYPTSABSGAMTUNFLKGERERILJOKKLYTDDNREPSTVETTVTAGETKGKIS
TYPPROGYPTSABSGAMTUNFLKORERILJOKATYDDNREPSTVETTVTTAGETKGKIS
OTKKEVAIKTTLKELYHKRVTPSEPDWAMOPDSYIEMMAQOGGENLLÄNTLETCTLTT
ARTKTAPDLILEKAETSKLTNFSLPDTRTCRIPAFHGWNYKVCHAICCVLNROGGKR
NYVLHGHGASTGKSIIAAAIAAANGCYNAANVNPPPROTYRKNILTWYBEAGNFGO
OVNOFKAICSGOTTADOKGKGSKOIEDPTVIMTUNNPPROTOTRINDILTWYBEAGNFGO
OVNOFKAICSGOTTADOKGKGSKOIEDPTVIMTUNNPPROTOTRINDILTOPINDIR
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/tb_xref="REMTREMBL:CAC39991"
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/tabalation="MAGNEMBL"
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/db_xref="E1:14273918"
/db_xref="EMTREWEBL:CAC39993"
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RMLNIHLTHTLPGDFGLVDKNEWPMICAWLVKNGYQSTWASYCAKWGKVPDWSENWAE
PKVPTPINLLGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAE
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TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
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Parvovirus nsl variants
Patent: EP 1077260-A 8 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts (DE)
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Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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                                                                                                                                                                                                               /note="unnamed protein product"
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                                                                                                                  /note="Parvovirus NS1 variant"
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/mol_type="unassigned DNA"
/db_xref="taxon:10794"
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/db_xref="G1:14273914"
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Sequence 8 from Patent EP1077260.
AX137743
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TITLE
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ORIGIN

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FEATURES

ORIGIN

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Minute virus of mice with two major open reading frames (genome).

Voll15

Voll15. GI:60911

coat protein; genome; origin of replication; overlanning frames.

Mice minut repeat.
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db_xref="G1:14273926"

/db_xref="REWTREMEL:CAC39997"

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NTKNIFPGDVNWFVQHEWGKDQGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRWLVTA
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SPRENGSTELSSDGWKTNELKEGERENLUSKLYTDDMRPETVETVTTAGETKRKRI
QTKKEVSIKTLKELVHKRYTSPEDWMMQDDSYIEWAQPGGENLLKNTLECTLTL
ARTKTAFDLILEKAETSKLINFSLPDTRICRIPAFHGWNYVKVCHAICCVLNRQGGKR
                                                                                                       QVNQPKAICSGQAIRIDĞKGKGSKQIEPTPVIMTTNENITVVRIGCEERPEHTQPIRĞ
MAINHLIHTHILGBGAUSVOKREWPHT (AMUVKYRĞYĞYRMASVOKKWĞKVPDWSEKWAE
PKVPPTPINLIGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAE
TQNTGBAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPINLD"
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Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Mice minute virus
Viruses; sgDMA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (Dases 1 to 5081)
                                                                                 1 ATTIGCTGTGTTTTAAACAGACAAGAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGACCA
                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                         ö
  Length 2019;
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                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                         Indels
                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58.4; DB 6;
Pred. No. 5e-08;
0; Mismatches 1;
  ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .2019
/note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Parvovirus NS1 variant"
Score 58.4; DB 6
Pred. No. 5e-08;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Mice minute virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   nsl variants
1077260-A 16 21-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="unassigned DNA"
/db xref="taxon:10794"
                                                                                                                                                                                                                          2019 bp
Sequence 16 from Patent EP1077260.
AX137751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             Nueesch, J. and Rommelaere, J.
                                                                                                                                                                                                                                                                                               AX137751.1 GI:14273925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.3%;
Query Match
Best Local Similarity 98.3%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .2019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parvovirus Patent: EP 1
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TITLE

FEATURES

COMMENT

SCO

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CRIEVANTTDTSVKGNMAKDDAHEQI WTPWSLVDANAWGVWLQPSDWQYI CNTWSQLN LVSLDQEI ENVVLKTYTEQDLGGQA.KI YNNDLLYACMVWGYDSNNI LLEYTPAANSWET LLGFPWRFT LLASPYRYPEVOEDRLSYYPENQGETVEHNWGYDRDS PKGI PQFFT IENTQQI TLLATGGDEPALGYYPETT TLLATGGOPPLLSTPPRADTDAGTLTAAQGSHGTTQWGVNWVSEAIRTRPAQVGFCQPHNDFEASRAGPFARDTDAGTLTAAQGSHGTTQWGVNWVSEAIRTRPAQVGFCQPHNDFEASRAGPFAAPKVPADITQGVDKEANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2383. .4551
/note="unnamed protein product; Protein sequence is in
conflict with the conceptual translation; coding sequence"
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/db_xref="SPTREMBL:Q84207"
/translat.ton="MHLVLGWVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDEAYDQY
IKSGKNPYLYFSAADQRFIDQTKDAKDWGGKVGHYFPRTKRAFAPKLATDSBEGTSGV
SRAGKRPPPPAYIFINQARAKKKLTSSAAQQSSQTMSDGTSQPDSGNAVHSAARVERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGSARSPETTPKSTPLSONYALTPLADLEDLALEPWSTPNTPVAGTAETONTGEAGS
KACQDGQLSPTWSE1EEDLRACFGAEPLKKDFSEPLNLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADGPGGSGGGGGGGVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENY
                                                                                                                                                The messenger RNA of this virus (colinear with the strand listed is spliced, but the exact splice sites are not known. The listed strand is complementary to the one which is included in the virion.
Astell, C.R., Thomson, M., Merchlinsky, M. and Ward, D.C.
The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2286. .2354
/note="unnamed protein product; coding sequence"
/codon_start=1
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codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                       'note="unnamed protein product; coding sequence"
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                                                                            Nucleic Acids Res. 11 (4), 999-1018 (1983)
                                                                                                                                                                                                                    1. .5081
/organism="Mice minute virus"
/mol_type="genomic DNA"
/db_xref="taxon:10794"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'translation="MFNYLFYRPEITWF"
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db xref="G1:60913"

db_xref="GOA:P03137"

db_xref="GOA:P03137"
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/db_xref="G1:584078"
/db_xref="SPTREMBL:Q89491"
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/db_xref="G1:60914"
/db_xref="SPTREMBL:Q89818"
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/proteIn_id="CAA24313.1"
/db_xref="GI:1335397"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA24309.1"
/db_xref="G1:60912"
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                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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                                                    parvovirus
                                                                                                         83143341
                                                                                                                                   6298737
                                                                                                                                                                                                                                                                 source
                                                                                                         MEDLINE
PUBMED
     AUTHORS
                                                                            JOURNAL
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CDS

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SVRYSYGKQHGENWASHGPAPERYTWDETSFGSGRDTKDGFIQSAPLVVPPPLNGILT
NANDIGTKMDDIHESNVFNSYGPLIAPERPSPYPYDPQQJWDKELDLEHKPRLHITAPFV
CKNNAPGQMIVRLGPNITDOYDPNGATLSRIVTYGTPFWKGKLTWRAKIRANTTWNPV
YQYSAEDNGASYMSYTKWLPTATGNMQSVPLITRPVARNTY
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                   VRL 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in mouse I (variant A-9) cells.
The parvoviridae family cantains two groups that infect mammalian hosts: (i) defective (helper-dependent) adeno-associated viruses, and (ii) autonomous (helper-independent) parvoviruses. MVM is a member of the latter group. Both groups have been demonstrated to gackage both plus and minus strands (in separate particles) of the ss-DNA genome, though the minus strand is more typically packaged in the latter group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treplication [1].

The left and right halves of the genome encode two distinct, but overlapping transcriptional units. The transcripts can be summarized [1] (1 map unit (mu) = 51 bp):

R1 (4.8 kb): 4.5 mu - 46 mu; 46 mu - 95 mu
R2 (3.3 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46 + mu - 95 mu
R3 (3.0 kb): 40 mu - 46 mu; 46 + mu - 95 mu
R3 is the major transcript.

R3 is the wajor open reading frames, both on the plus (or C) There are two major open reading frames, both on the plus (or C) after and. The left side ORF (261-2279) probably encodes a non-capsid protein of 85 kd; the right side ORF probably encodes the viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence below corresponds to the plus (+) strand, also referred to as the C-strand. The minus (-) strand is also referred to as the V-strand.

The 3' and 5' termini both exhibit the potential for forming stable 'fold-back' hairpins; these sequences appear to play a role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Three splicing patterns are used to excise the small intron common to all minute virus of mice RNAs J. virol. 60 (3), 1170-1174 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Original source text: Minute virus of mice (strain MVM(p)), passed
                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Astell, C.R., Thomson, M., Merchlinsky, M. and Ward, D.C.
The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 5149)
Astell,C.R., Gardiner,E.M. and Tattersall,P.
DNA sequence of the lymphotropic variant of minute virus of mice
NVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (bases 1 to 5149)
                                                                                                                                                                                                                                                                                    1 ATTTGCTGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGACCA
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                             ö
                                                                                                                                                                   97.3%; Score 58.4; DB 14; Length 5081; 98.3%; Pred. No. 4.9e-08; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minute virus of mice, complete genome.
JO2275 MIS220 MI2521 M14704
JO2275.1 GI:332293
alternative splicing; capsid protein; complete genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5149 bp ss-DNA
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J. Virol. 57 (2), 656-669 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morgan, W.R. and Ward, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nonstructural protein.
Mice minute virus
Mice minute virus
                                                                                                                                                                                                                                   59; Conservative
                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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AUTHORS
TITLE
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TITLE
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TITLE
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VERSION
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GTSGVSRAGKRTRPPAYIFINQARAKKKLTSSAAQQSSQTMSDGTSQPDSGNAVHSAA
RVERAADGPGGSGGGGGGGGVGVSTGSYDNQTHYRPLGDGWVEITALATRLVHLNMP
KSENYCRIRVHNTTDTSVKGNMAKDDAHEQIWTPWSLVDANAWGVWLQPSDWQYICNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGTTQMGVNWVSEAIRTRPA
QVGFCQPHNDFEASRAGPFAAPKVFADITQGVDKEANGSVRYSYGKQHGENWASHGPA
                                                                                                                                                                                                                                                                                                                                                                                                       MSQLNIJSLDQEI FNVVLKTVTEQDLGGQAIKI YNNDLTACMMVAVDSNNI LEYTPAA
NSMETLGFYPWKPTI ASPFYX FYCMDRDLSYTYENQEGTPHVWGTPREMNSGPFTI
NSTOGI TILRATGDEFATGTYX FYTRAWYKLTHTWQTNRQLGQPPLLSTFPEADTDAGTI
TAQGSRHGTTQMGVNWYSEAIKTPRAQVGFCQPNDFFASRAGPFAAPKVPADITQGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGQAIKIYNNDLTACMMVAVDSNNILPYTPAANSMETLGFYPWKPTIASPYRYYFCVD
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GPLTAFSHPSPVYPQGQIWDKELDLEHKPRLHITAPFVCKNNAPGQMLVRLGPNLTDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKEANGSVRYSYGKOHGENWASHGPAPERYTWDETSFGSGRDTKDGFIQSAPLVVPPP
LIGILIVNAN PIGTKNDI HFSNVFNYSVGSPLTARSHPSPYVEROĞQÎ WÜKELDLEHKPRLH
LIGILIVNA PIGYLNILGEPKLTDOYDPNGATLSRI VYTYGTFFWKGKLTWRAKLRAN
TTWNPVYQVSAEDNGNSYMSVTKWLPTATGNMQSVPLITRPVARNTY"
                                                                                                                                                                                                                                                                         /translation="MAPPAKRAKRGWVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDE
                                                                                                                                                                                                                                                                                                    AYDQYIKSGKNPYLYFSAADQRFIDQTKDAKDWGGKVGHYFFRTKRAFAPKLATDSEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein id="AAA67110.1"
/db_xref="GI:825482"
/translation="MAPPAKRAKRGKGLRDGWLVGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14;
                                                   /note="alternative intron"
join(2286. .2316,2399. .4557)
/gene="VP1"
                                                                                                                                      join(2286. .2316,2399. .4557)
gene="VP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MFNYLFYRPEITWF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="unknown protein"
protein_id="AAA67112.1"
/db_xref="G1:825483"
/translation="MVGWWGINV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="unknown protein"
/protein_id="AAA67113.1"
/db_xref="GI:825484"
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                                                                                                                                                                                                                        /proteIn_id="AAA67111.1"
/db_xref="GI:332294"
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/gene="VP"
/note="VP intron (alt.)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="ORF1; putative"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2332. .2361
/gene="VP"
/note="ORF3; putative"
/codon_start=1
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/codon_start=1
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/gene="VP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2286. .2354
/gene="VP"
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/gene="VP"
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/gene="VP1"
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RMLNIHLTHTLPGDFGLVDKNEWPMICAWLVKNGYQSTWASYCAKWGKVPDWSENWAE
PKVPTPINLLGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAE
TONTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="Misgsgslnogakrkwawfkvykollksvyylffhsvsrdake
Snoltmagnaysdevlcatnwlkeksnoevfsfvfknenvolngkdigwnsykkelob
Delkslorgaettwdosedmewettvdewtkkovfifdslvkkclffevlnyknifpgd
Vnwfvohewgkdoggmhchvliggkdfsqaggkmwrrolnvywsrwlvyacnvollfpab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKLREIAEDNEWYTLLTYKHKOTKKOYTKCYLFGNM AYYFLTKKKISTSPPROGGY
FLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRIQTKKEVSIK
TTLKELVHKRVTSPEDWMMQPDSYIEMMAQPGGENLLKNTLEICTLTLARTKTAFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSYKKELQEDELKSLQRGAETTWDQSEDMEWETTVDEMTKKQVF1FDSLVKKCLFEVL
NTKN1 FPGDVNWFVQHEWGKDQGWHCHVL1GGKDFSQAQGKWWRRQLNVYWSRWLVTA
CNVQLTPAER1KLRE1AEDNEWVTLLTYKHKQTKKDYTKCVLFGNM1AYYFLTKKKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTKKEVSIKTTLKELVHKRVTSPEDMMMQPDSYIEMMAQPGGENLLKNTLEICTLTL
ARTKTAFDLILEKAETSKLTNFSLPDTRTCRIFAFHGMNYVKVCHAICCVLNRQGGKR
NTVLFHGPASTGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAGNFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="G1:332295"
/translation="MAGNAYSDEVLGATNWLKEKSNQEVFSFVFKNENVQLNGKDIGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILEKAETSKLTNFSLPDTRTCRIFAFHGWNYVKVCHAICCVLNRQGGKRNTVLFHGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAGNFGQQVNQFKAIC
SGQTIRIDQKGKGSKQIBPTPVIMTTNENITVVRIGCEERPEHTQPIRDRMLNIHLTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
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capsid proteins, VPI (or A, 83 kd), VP2 (or B, 64 kd), and VP3 (or C, 61 kd). But because of uncertainties about the precise splice points in the transcripts, the exact starts, stops and (possible) intron boundaries are not known.

revision 4804 4870 a-65bp-a in [2]; aa in [1] [2]

revises [1].
[3] sites; splice sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLPGDFGLVDKNEWPMICAWLVKNGYQSTMASYCAKWGKVPDWSENWAEPKVPTPINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
                                                                                                                                                                                                                                                                                                                          /db xref="taxon:10794"
/lab_host="mouse 1 (variant A-9) cell"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="nonstructural protein"
/protein_id="AAA67108.1"
/db_xref="G1:825481"
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/product="nonstructural_protein"
/protein_id="AAA67109.1"
                                                                                                                                                                                                                                           /organism="Mice minute virus"
/mol_type="genomic DNA"
/strain="MVM(p)"
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/gene="VP"
/note="alternative intron"
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1. .5149
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/gene="NS1"
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/gene="NS1"
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/gene="VP"
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/gene="NS1"
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/gene="VP"
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/gene="VP"
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/gene="NS1"
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U34255.1 GI:1464792
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Besselsen, D.G.
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Hamster parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 96.7
Matches 58; Conservative
                                                                                                                  Best Local Similarity
Matches 58; Conserv
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HOU34255
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KEYWORDS
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MOU34254
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Mouse parvovirus 1b
Viruges; ssDNA viruses; Parvoviridae; Parvovirus.
Viruges; ssDNA viruses; Parvoviridae; Parvovirus.
1 (bases 1 to 4764)
1 (bases 1 to 4764)
1 (bases 1 to 400k, R. R. Jr. and Riley, L. K.
Franklin, C. L., Hook, R. R. Jr. and Riley, L. K.
Franklin, C. L., Hook, R. R. Jr. and Riley, L. K.
J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
                ö
                                                              VRL 21-AUG-1996
                                                                                                                                                                                                                                        Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

1 (bases 1 to 4761)
Besselsen, D.G., Pintel, D.G., Purdy, G.A., Besch-Williford, C.L., Frantlin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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                 Gaps
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Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pathology, University of Missouri-Columbia, W213
Veterinary Medicine Building, Columbia, MO 65211, USA
Location/Qualifiers
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Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pathology, University of Missouri-Columbia, W213
Veterinary Medicine Building, Columbia, MO 65211, USA
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94.7%; Score 56.8; DB 14; Length 4761;

Best Local Similarity 96.7%; Pred. No. 1.6e-07;

Matches 58; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                       linear
                1; Indels
                                              1 ATTIGCIGIGITITIAAACAGACAAAGGAGGCAAAAAGAAAIGCIGITII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /specific_host="Mesocricetus auratus"
/db_xref="taxon:10794"
Pred. No. 4.9e-08;
0; Mismatches 1
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                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mice minute virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="Cutter"
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                                                                                                                                                                      Mice minute virus DNA. U34256
 Similarity 98.3%;
59; Conservative
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desselsen, D.G.
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Besselsen, D.G.
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Mice minute virus
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   Best Local
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1 (bases 1 to 4773)
Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Franklin, C.L., Hook, R.R. jr. and Riley, L.K.
J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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Mouse parvovirus 1c
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (bases 1 to 4.7).
Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses
J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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                                                                                                                                                                                                                      ö
                                                                                                                                                                    94.7%; Score 56.8; DB 14; Length 4764;
llarity 96.7%; Pred. No. 1.6e-07;
Conservative 0; Mismatches 2; Indels 0;
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|specific host="Mus musculus"
|db_xref="texon:42842"

    .4764
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/gene="VPl"
/codon_gtart-
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J. Virol. 570, 656-669 (1986)
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/note="putative"
/codon_start=1
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1 Similarity 96.7%;
58; Conservative (
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115. .2280
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TSPPRDGGYFLSSDSGWKTNFLKEGERHLYSKLYTDDNR PETVETYTYTAĞETKEKIS
OTKKEVSIKTILKELVHKYTSFDROMMANQPDSYIEMAQPGGBNLLKNTLETCTLTT
ARTKTAFDLILEKAFSFKLTNFSELPDNFRTCKIFAFHGWNYIKVGFAR
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VNOPKALIGSGQTIRIDQKGKGKSKQIEBTPVLINTBAITVRAIGSEBEHOPIRD
RMIAIHLTHTLPGDFGLVDKNEWPMICAMLYKNGYOSTWASYCAKWGKVPDWTENWAE
PKVPTPINSLGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTFVAGTAE
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Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
1 (bases to 5144)
Ball-Goodrich, L. J. and Johnson, E.
Molecular characterization of a newly recognized mouse parvovirus virus. 68 (10), 6476-6486 (1994)
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W213
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join(2290. .2320,2403. .4561)
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                                                                       Direct Submission
Submitted (17-AUG-1995) David G. Besselsen, Department
Veterinary Pathology, University of Missouri-Columbia,
Veterinary Medicine Building, Columbia, MO 65211, USA
Location/Qualifiers
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                                                                                                                                                                                                                             1. .4773
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/organism="Mouse parvovirus 1"
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/gene="NS1"
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                2 (bases 1 to 4773)
Besselsen, D.G.
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Ball-Goodrich, L.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56.8; DB 14;
Pred. No. 1.6e-07;
0; Mismatches 2;
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                      STGKSI I AQALAQAVGNVGCYNAANYNFPFNDCTNKNILIWVEEAGNFGQQVNQFKAIC
SGQTI KI DONGKGSKQI EPFPVIMTNBN ITVVR I GCBERPBHTQPI RDRMLAIHLTH
TLFGDFGLVOKNEWPMI CAMLVKNGYGSTMAS YCAKMGKVPDWSENWAEPKVPTPINS
LGSARS PFTTPKKTPKNTAITPLASDLEDIALEPWSTPNTPVAGTAETQNTGEAGG
KACQDGQLSPTWSE I EEDLRACFGAEPLKRDFSEPLINLD"
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GTSGVSRAGKRTRPPAYIFINQARAKKKLTSSAAQQSSQTMSDGTSQPDGGNAVHSAA
RVERAADGPGGSGGGGGGGVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMP
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DREANGSVRYSYGKQHGENWAAHGPAPERYTWDETNFGSGRDTRDGFIQSAPLVVPPP
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I LEKAETSKLTNFSLPDTRTCKI FAFHGWNYVKVCHAI CCVLNRQGGKRNTVLFHGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARTKTAFDLI LEKAETSKLTNFSLPDTRTCKI FAFHGWNYVKVCHAI CCVLMRQGGKR
NTVLFHGPASTGKSI I AQAI AQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAGNFGQ
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MSQLNLVSLDQEI FNVVLKTVTEQDSGGQAI KI YNNDLTACMMVAVDSNNI LPYTPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITAPFVCKNNAPGQMLVRLGPNLTDQYDPNGATLSRIVTYĞTFFWKGKLTMRAKLRAN
ITWNPVYQVSVEDNGNSYMSVTKWLPTATGNMQSVPLITRPVARNTY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTKKEVSIKTTLKELVHKRVTSPEDWMMMQPDSYIEMMAQPGGENLLKNTLEICTLTL
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ENTQQ I TLLKTGDEFATGTYYFDTNPVKLTHTWQTNRQLGQPPLLSTFPEADTDAGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PONTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKRDFSEPLNLD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="major transcription start site"
                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product="nonstructural protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Join(2287, .2317,2400, .4558)
/gene="VP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(2287. .2317,2400. .4558)
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gene="VP"
'note="alternative intron"
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                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAA69567.1"
/db_xref="GI:332291"
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'db_xref="GI:332290"
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/note="ORF1; putative"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ∠vu/. .2281
/gene="VP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="minor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="minor
                                                                                                                                                                                      201. .>2280
/gene="NS1"
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/gene="VP"
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'gene="VP"
                                                                                                                                                                                                                                                                                                              gene="NS1"
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coat protein; genome; origin of replication; overlapping genes; terminal repeat; unidentified reading frame.

Mice minute virus
Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

1 (Bases I to 5087)
Sahli,R., McMaster,G.K. and Hirt,B.

DNA sequence comparison between two tissue-specific variants of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAMYMI 5087 bp DNA linear VRL 01-JUL-1999
Mouse parvovirus minute virus immunosuppressive variant genome ( =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCRIRVHNTTDTSVKGNMAKDD
AHEQIWTPWSLVDANAWGVWLQPSDWQYICNTWSQLNLVSLDQEIFNVVLKTVTEQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGQAIKIYNNDLTACMAVAVDSNNILPYTPAANSMETLGFYPWKPTIASPYRYYFCVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rdlsvtyenqegtiehnvmgtpkgmnsqfftientoqittlrtgdefatgtyyfdtnp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATQMEVNWVSEAIRTRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVGFCQPHNDFEASRAGPFAAPKVPADVTQGVDREANGSVRYSYGKQHGENWAAHGPA
RERYTWDETNFGSGRDTREDGFLQSAPLVVPPPLANGILINNANDIGTKNDIHESNVFNSY
GPLTAFSHPSPYYGGGZIMVKELDLEHKPRLHITAPPVCKNNAPGQMIVRLGPNLTDO
YDPNGATLSRIVTYGTFFWKGKLITMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKMLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MSDGTSQPDGGNAVHSAARVERAADGPGGSGGGGGGGGGVGVST"
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/product="unknown protein"
/protein id="AAA69568.1"
/db_xref="GI:825478"
/translation="MAPPAKRAKRGKGLRDGWLVGY"
<2287. .2317
/gene="VP1"
/number=2
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2355. .2399
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'db_xref="GI:825480"
                                                                                                                                                                                                                'note="alternative intron'
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                                                                                                                                                                                                                              2333. .2362
/gene="VP1"
/note="ORF3; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="VP1"
/note="ORF2; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="GI:332292'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                     codon start=1
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/protein_id="A
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/gene="VP2"
2795. .4558
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                                                                                                                                                                    2318. .2399
/gene="VP1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'number=2
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ORGANISM
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Matches
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AUTHORS
TITLE
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PAMVMI
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KEYWORDS
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TKODI HFSNVFNSYGPLTAFSHPSPVY PQGQI WDKELDLEHKPRLHI TAPFVCKNNAP
GQML VRLGPNLTDQY DPNGATLSRI VTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVE
DNGNSYMSVTKWLPTATGNMQSVPLI TRPVARNTY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRDLSVTYENQEGTI EHNVMGTPKGMNSQFFTI ENTQQI TLLRTGDEFATGTYYFDTN
PVKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATQMEVNWVSEAI RTRP
AQVGFCQPHNDFEASRAGPFAAPKVPADVTQGVDREANGSVRYSYGKQHGENWAAHGP
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YGPLTAFSHPSPVYPQGQIWDKELDLEHKPRLHITAPFVCKNNAPGQMLVRLGPNLTD
QYDPNGATLSRIVTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTIASPYRYYFCVDRDLSVTYENQEGTIEHNVMGTPKGMNSQFFTIENTQQITLLRTG
DEFATGTYYFDTNPVKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATQM
EVNWVSEAIRTRPAQVGFCQPHNDFEASRAGPPAAPKVPADVTQGVDREANGSVRYSY
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DAHEQIWTPWSLVDANAWGVWLQPSDWQYICNTMSQLNLVSLDQEIFNVVLKTVTEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPPAYIFINQARAKKKLTSSAAQQSSQTMSDGTSQPDGGNGVHSAARVERAADGPGGS
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| FNVVLKTVTEQDSGGQAIKI YNNDLTACMMYAVDSNN I LPYTPAANSMETLGFYPWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKOHGENWAAHGPAPERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGILTNANPIG
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                                                                                                                For the fibroblast-specific strain (MVMp) sequence see <PAMWM2>.

The genomes of MVMp and MVMi (immunosuppressive variant) have more than 96% of their sequence in common.

Data kindly reviewed (IB-UUL-1986) by G. McMaster.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="VPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDEAYDQYIKSGKNF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLYFSAADQRFIDQTKDAKDWGGKVGHYFFRTKRAFAPKLATDSEPGTSGVSRAGK
autonomous parvovirus, minute virus of mice
Nucleic Acids Res. 13 (10), 3617-3633 (1985)
85242059
3855242
                                                                                                                                                                                                                                                                                                                                                                                                                  note="terminal hairpin region"
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'note="polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="polyadenylation signal"
                                                                                                                                                                                                                                                                                        /organism="Mice minute virus"
/mol_type="genomic DNA"
/db_xref="taxon:10794"
1. _116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             xref="GOA:P07302"
xref="SWISS-PROT:P07302"
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/db_xref="Gl:5419928"
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/db_xref="GI:5419929"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="coat protein"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xref="GOA:P07302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="TATA box"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <2405. .4558
/gene="VP1"
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/gene="VP2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2405. .4558
/gene="VP1"
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92.0%; Score 55.2; DB 14; Length 5087; 95.0%; Pred. No. 4.9e-07;

Query Match Best Local Similarity

Search completed: June 2, 2004, 18:58:36 Job time : 652 secs

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Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.

DNA trans

AAS45354 AAS46367 ABK28187

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                                 The present sequence is a parvovirus non-structure protein (NSI) variant (T394A) DNA fragment. The invention relates to the variants of the parvovirus non-structure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                        1 ATTTGCTGTGTTTTAAACAGACAAGAGGCAAAAGAAATGCTGTTTTATTTCATGGACCA 60
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/*tag= a
/product= "NS1 variant (T394A) protein"
replace(1180, A)
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                                                                                                                              Sequence 60 BP; 20 A; 8 C; 13 G; 19 T; 0 U; 0 Other;
               Disclosure; Page 21-22; 41pp; English.
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97.3%; Score 58.4; DB 5; Length 2019;
Best Local Similarity 98.3%; Pred. No. 1.7e-09;
Matches 59; Conservative 0; Mismatches 1; Indels 0
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31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                              AAD02801;
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The present sequence is a wild type DNA encoding parvovirus nonstructure protein 1 (NS1). The present invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                NSI; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 97.3%; Score 58.4; DB 5; Length 2019; 1. Similarity 98.3%; Pred. No. 1.7e-09; 59; Conservative 0; Mismatches 1: Indele 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parvovirus non-structure protein 1 (NS1) variant (S283A) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2019 BP; 698 A; 389 C; 452 G; 480 T; 0 U; 0 Other;
                                                                              Parvovirus non-structure protein 1 (NS1) wild-type DNA
                                                                                                                                                                                                                                                                           /product= "Parvovirus NS1 protein"
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                                                                                                                                                                                                                 Location/Qualifiers
1. .2019
/*tag= a
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                                            (first entry)
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                        (revised)
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P-PSDB; AAY72702.
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Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                 EP1077260-A1
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                        06-AUG-2003
31-MAY-2001
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31-MAY-2001
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                                                                                                                                                                               Parvovirus
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AAD02799
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1141 ATTTGCTGTGTTTTAAACAGACGAAGAAGAAAAAAAATACTGTTTTATTTCATGGACCA 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a DNA encoding parvovirus non-structure protein (NSI) variant (T463A). The invention relates to the variants of the parvovirus non-structure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cyclocoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                           NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
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                                                                                                                                                                                                                                                         Parvovirus non-structure protein 1 (NS1) variant (T463A) DNA.
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/product= "NS1 variant (T463A) protein"
replace(1387, A)
/*tag= b
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1. .2019
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                                                                                                                      AAD02805 standard; DNA; 2019
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                                                                                                                                                                                                 (revised)
(first entry)
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31-MAY-2001
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Synthetic

mutation

AAD02805;

AAD0280 RESULT

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Gaps ô 9

Parvovirus Synthetic

AAD02797 standard; DNA; 2019 BP

RESULT 5
AAD02797
ID AAD0
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AAD02797

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Query Match

Matches

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Gaps

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mutation

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This viral DNA is isolated from a non- attenuated CPV. The DNA is preferably derived from vB1440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pGEM3Z or pGEM5Z. The host cells to be transfected ar selected from Norden Liaboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells or canine A72 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parvovirus; dog; vaccine; CPV; myocardial disease; enteric disease; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Attenuated CPV strains contg. up to 4 mutation (s) relative to control virus - useful as a veterinary vaccine against CPV disease in animals, such as wild or domestic dogs.
                                       Attenuated CPV strains contg. up to 4 mutation (8) relative to control virus - useful as a veterinary vaccine against CPV disease in animals, such as wild or domestic dogs.
                                                                                                                                                                                                                                                                                                                                                                            1422 TGTGTTTTTAAATAGACAAGGTGGTAAAAGAAATACAGTTCTTTTTCATGGACCA 1475
                                                                                                                                                                                                                                                                                                                                               7 TGTGTTTTAAACAGGACAAGGGCAAAAGAAATGCTGTTTTATTTCATGGACCA
                                                                                                                                                                                                                                                Sequence 5049 BP; 1791 A; 812 C; 1029 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                 Length 5049;
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                                                                                                                                                                                                                                                                               Score 42.8; DB 2;
Pred. No. 0.00027;
0; Mismatches 7;
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                                                                                                         Claim 1; Page 21-24; 42pp; English.
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Best Local Similarity 87.0%;
Matches 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canine parvovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
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                                  /*tag= a
/product= "NS1 variant (S283A) protein"
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                                                                                                                                                                                                                                                                                                                                                                                 transcription activities, and cytotoxic activity.
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 Location/Qualifiers
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                                                                                                                                                                                                                                                                         Nueesch J, Rommelaere J;
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AAT15311

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15-MAY-1996;
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feline
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Matches
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8
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                                                                       This viral DNA is isolated from an attenuated CPV. The DNA is preferably derived from vB1440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pGEM3Z or pGEM5Z. The host cells to be transfected ar selected from Norden Laboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   //note = "base 4358 is C in virulent CPV-39 (T in passage
65 attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/note= "base 4307 is A in virulent CPV-39 (G in passage
65 attenuated virus)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in passage
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                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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feline panleukopenia virus; mink enteritis virus; infection; ds
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                                                                                                                                                                                                                                                                        Sequence 5049 BP; 1790 A; 814 C; 1029 G; 1416 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                              Length 5049;
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/note= "base 4889 is C in virulent CPV-39
65 attenuated virus)"
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/note= "base 4409 is C in virulent CPV-39
65 attenuated virus)"
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attenuated virus"
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                                                                                                                                                                                                                                                                                                                           71.3%; Score 42.8; DB 2;
87.0%; Pred. No. 0.00027;
tive 0; Mismatches 7;
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/note= "NS1/NS2 coding region"
2286. .4541
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/note= "VP1/VP2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Attenuated canine parvovirus genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                         Claim 2; Page 24-27; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
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                                                                                                                                                                                                                                                                                                                                                  Local Similarity 87.0 les 47; Conservative
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AAT88321
AAT
X & X & S & S & S & S & S & S & S
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Canine parvovirus DNA carrying specific attenuating mutation(s) - used as vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Attendated viruses are obtained by serial passage of the virulent CPV type 2b isolate 39 in NLFK feline kidney host cells. They have one or more of the sequence relaterations indicated in the sequence relative to the sequence relative to a claimed virus from the 65th passage) wild-type CPV-2b (see AAT88320). A claimed virus from the 65th passage (deposited as ATCC VR 2528) contains all 6 mutations. The DNA from attenuated CPV strains (see also AAT88324) is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks of the virus. The attenuated viruses can be used in dogs as a vaccine to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protect against CPV disease, or more generally in cats and minks to protect against feline panleukopenia virus and mink enteritis virus. The vaccines protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), providing a long term immune response. (NB. this sequence was created by adaptation of the wild-type CPV-2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This DNA molecule encodes an annenuated canine parvovirus (CPV) genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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panleukopenia virus; mink enteritis virus; infection; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 71.3%; Score 42.8; DB 2; Length 5049; Local Similarity 87.0%; Pred. No. 0.00027; les 47; Conservative 0; Mismatches 7; Indels 0
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"base 59 is G in CPV-39 (passage 5)"
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/note= "VP1/VP2 coding region"
4745
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                                                                                                                                            Carmichael LE, Gruenberg A;
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"base 97 is
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                                                                      (CORR ) CORNELL RES FOUND INC
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96US-00647655
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page; 60pp; English
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/note=
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20-NOV-1997.

mutation

us-10-069-056-11.rng

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24-OCT-2003
12-JAN-1992
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                                                                                                                                           WO9742972-A1
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Matches
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Key
                                                                       CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               This DNA sequence comprises an attenuated virus genome derived by serial passaging (60 times) of virulent canine parvovirus (CPV) type 2b isolate passaging (60 times) of virulent canine parvovirus (CPV) type 2b isolate (59 in NLFK feline kidney host cells. The attenuated virus is designated companies to the sequence (see AAT88320) of the control (5th passage) wild-type CPV-2b. 2 Mutations (see AAT88320) of the control (5th passage) wild-type CPV-2b. 2 Mutations can michin the hairpin formed by the 3' terminal palindrome: the mutation cc at nucleotide 59 introduces an A into a G-C rich region within the tip of the hairpin, disrupting the base pairing in one of the 2 small internal cc palindromes within that sequence; the thymine at nucleotide 97 is adjacent to the mismatched bubble (filp-flop) sequence within the cycle adjacent to the mismatched bubble (filp-flop) sequence within the CC adjacent to the mismatched bubble (filp-flop) sequence within the cut an betanated viruses can be used in dogs as a vaccine to protect against CPV disease, or more generally in cats and minks to protect against the currently prevalent cpt and mink the vaccines correct against the currently prevalent cpt correctines can be used in dogs and all extant correct squainst the currently prevalent cpt cut catains of types 2 and 2a), providing a long term immune response.
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                                                                                                                                                                                                                                                                                                                                                               Canine parvovirus DNA carrying specific attenuating mutation(8) - used as vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1422 TGTGTTTTAAATAGACAAGGGGTAAAAGAAATACAGTTCTTTTCATGGACCA 1475
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feline panleukopenia virus; mink enteritis virus; infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 TGTGTTTTAAACAGACGAGGGGGCAAAAGAAATGCTGTTTTATTTCATGGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5049 BP; 1791 A; 812 C; 1029 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.3%; Score 42.8; DB 2; Length 5049; 87.0%; Pred. No. 0.00027; tive 0; Mismatches 7; Indels 0;
                    "base 4745 is T in CPV-39 (passage 5)"
                                                                /*tag= f
/note= "base 4881 is C in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canine parvovirus 39 passage #5 (wild-type).
                                                                                                                                                                                                                                                                                                Gruenberg A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canine parvovirus; type 2b isolate 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Page 34-37; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT88320 standard; DNA; 5049 BP
                                                                                                                                                                                                                                                           (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                           96US-00647655.
                                                                                                                                                                                       97WO-US007584
                                                                                                                                                                                                                                                                                                Parrish CR, Carmichael LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.0°
Matches 47; Conservative
           Φ
           /*tag=
/note= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                    WPI; 1998-008583/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-0CT-2003
21-MAY-1998
                                                                                                                                                                                          36-MAY-1997;
                                                                                                                   WO9742972-A1
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AAT88320;

RESULT 11 AAT88320

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This DNA sequence comprises the genome of virulent canine parvovirus type 2b (CPV-2b) isolate 39, obtained after 5 serial passages in NLFK feline 2b (CPV-2b) isolate 39, obtained after 5 serial passages in NLFK feline 2c (ArCC VR 2489) (see AAT88324) from the 60th passage, and a claimed virus (ArCC VR 2489) (see AAT88324) from the 60th passage, and a claimed virus (see AAT88321) derived from the 65th passage (ATCC 2528). These cespectively contain 4 and 6 mutations in comparison to the virulent 5th passage virus. The DNA from attenuated CPV-2b strains is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks of the virus. The cyclostic can be used in dogs as a vaccine to protect against the unce generally in cats and mink to protect against CPV disease, or more generally in cats and mink to protect against claims and wink enteritis virus. The vaccines protect against cromains virus and mink enteritis virus. The vaccines protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), and provide a long term immune response. (Updated on 17-007-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canine parvovirus DNA carrying specific attenuating mutation(s) - used as vaccines for protection against parvovirus and feline pan-leukopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1422 IGIGITITIAAATAGACAGGTGGTAAAAGAAATACAGTICTITITICATGGACCA 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence from the double-stranded replicative form DNA of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 TGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5049 BP; 1789 A; 813 C; 1030 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 5049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein envelope; immunogen; vaccine; antigen; epitope; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 11.3%; Score 42.8; DB 2; Local Similarity 87.0%; Pred. No. 0.00027; Nes 47; Conservative 0; Mismatches 7;
                                                                                                                                                                                            /*tag= b
/note= "VP1/VP2 coding region"
Location/Qualifiers
273. .2379
/*tag= a
/note= "NS1/NS2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porcine parvovirus; NADL-2 virulent strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gruenberg A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 8; Page 37-40; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .2073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAN40252 standard; DNA; 3524 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US007584.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carmichael LE,
                                                                                                                                                      .4541
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                                                                                                                                                              2286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-008583/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus infections.
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SOS

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The invention relates to a number of isolated Arabidopsis thaliana CDNA sequences and their encoded proteins which are especially transcription factor related CDNA's and proteins. The isolated or recombinant plant transcription factor polymuclectides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or alteration in a plant growth characteristic, e.g. growth such as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polymucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the CDNAs of the invention.
                                                                                                                                  New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493 ATTTGCAGAGTGTTCAATAAACAGGAGACAGAAAAATGTTGGATTAATCCAT 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
                    Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATTTGCTGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genomic polynucleotide SEQ ID NO 28579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Length 1005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1005 BP; 297 A; 244 C; 223 G; 241 T; 0 U; 0 Other;
                  Pineda O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 28579; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
Dubell AT,
                    Creelman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28.4; DB Pred. No. 11; 0; Mismatches
                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 446; 454pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
  Adam LJ,
                    Reuber TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL25702 standard; DNA; 2675 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 47.3%;
Local Similarity 70.4%;
es 38; Conservative
Riechmann JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                  Jiang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M,
                                                                            2003-248221/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY
                                                                            WPI; 2003-248221/
P-PSDB; ADD30418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200171042-A2
Ratcliffe O,
Pilgrim ML,
                                                                                                                                                                                                or apomixis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2001
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                                          Broun PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL25702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ទ
                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptide obtd. by recombinant DNA methods - for vaccination against parvovirus infections in man and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              development of vaccinal immunity against parvovirus infection. Also claimed are DNA sequences wholly or partly duplicative of defined sequences. The polypeptides are used in vaccines for conferring protection against parvovirus infections in man and animals. (Updated 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds; transcription factor; transgenic plant; growth rate; senescence; seed germination rate; plant vigor; seedling vigor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The inventors claim an immunologicallý active polypeptide for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3524 BP; 1400 A; 719 C; 648 G; 757 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1157 rgaaacagacaagagaaaaagaaaracaarrcrarrcarg 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant yield-related polynucleotide clone G2181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Table II, Page 33-49; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
  *tag= a
note= "see AAP40306"
107. .3522
                                                        /*tag= b
/note= "see AAP40675"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD30417 standard; cDNA; 1005 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-NOV-2001; 2001US-0336049P.
11-DEC-2001; 2001US-0338692P.
14-JUN-2002; 2002US-00171468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2002; 2002WO-US025805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001; 2001US-0310847P
                                                                                                                                                                                            84WO-US000063
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                                                                                                                                                                                                                                83US-00459203
                                                                                                                                                                                                                                                  84US-00567968
                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAP40306, AAP40675.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                  WPI; 1984-201354/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003013227-A2
                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN
                                                                                                                                                                                            19-JAN-1984;
                                                                                                                                                                                                                                19-JAN-1983;
                                                                                                                                                                                                                                                    06-JAN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JAN-2004
                                                                                                                  WO8402847-A
                                                                                                                                                    02-AUG-1984
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RESULT 13

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ADD30417

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABP72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Sequence 2675 BP; 728 A; 558 C; 654 G; 735 T; 0 U; 0 Other;

ö Gaps ö 57 DB 4; Length 2675; 13; Indels 0; Mismatches Score 28.2; I Pred. No. 15; 47.0%; Query Match, Best Local Similarity 73.5 Matches 36; Conservative

9 TGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGA ò g

ABL25700 standard; DNA; 3049 ABL25700; RESULT 15 ABL25700 

(first entry) 26-MAR-2002 Drosophila melanogaster genomic polynucleotide SEQ ID NO 28573.

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds

Drosophila melanogaster.

WO200171042-A2

27-SEP-2001

23-MAR-2001; 2001WO-US009231

23-MAR-2000; 2000US-0191637P 11-JUL-2000; 2000US-00614150

(PEKE ) PE CORP NY

Myers EW Li PWD, Venter JC, Adams M,

WPI; 2001-656860/75

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions

Claim 1; SEQ ID NO 28573; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 3049 BP; 767 A; 685 C; 765 G; 832 T; 0 U; 0 Other;

Query Match

DB 4; Length 3049; 47.0%; Score 28.2;

ö Gaps ; 0 741 TATTITTAAAAGCCCAGTAGGTACAAGGAATGATTTTCTATCTCATGGA 789 13; Indels 9 TGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGT Pred. No. 16; 0; Mismatches 73.5%; 36; Conservative Best Local Similarity Matches 36; Conserv g ઠે

2, 2004, 19:08:33 Search completed: June Job time : 148.25 secs

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5 28.2 47.0 536 12 BIS90311 6 28.2 47.0 538 13 BU397481 7 28.2 47.0 595 29 CE031004	, 26.2 4'.0 555 25 CECLIDUA 8 28 46.7 446 10 BE722343 9 28 46.7 518 13 BQ427038 10 27.8 46.3 303 10 BF401923	c 11 27.8 46.3 45.9 AA-110811 AA-110811 vt93d02.r c 12 27.8 46.3 468 9 AA-981917 AA-991917 ua34d03.r c 13 27.8 46.3 468 9 AA-089795 AA-09795 Vg2sa09.r c 14 27.8 46.3 541 10 AW-499334 AW-499334 660053A04	15 27.8 46.3 608 9 A1665130 16 27.8 46.3 652 28 BH199980 17 27.8 46.3 652 10 BB617491 18 27.8 46.3 727 28 BZ095363	27.8 46.3 748 29 CE213729 27.6 46.0 358 28 AQ102012 27.6 46.0 468 28 AZ283532	22 27.6 46.0 618 28 AZB103/8 23 27.6 46.0 718 28 AZB40364 24 27 4 46.0 829 12 RG167173	25 27.6 46.0 1201 9 AL561004 26 27.4 45.7 447 12 BT297026	27.4 45.7 584 13 BU094210 27.4 45.7 664 28 BZ243507 27.4 45.7 664 29 CECGO160	29 27.4 45.7 632 29 CE692156 31 27.4 45.7 790 12 BG936597 32 27.2 45.3 552 12 BI568163	27 45.0 55.0 14 CAS925364 27 45.0 55.0 14 CAS92583 27 45.0 55.1 9 AV915273 27 45.0 555.10 RF618681	27 45.0 601 10 BE060272 27 45.0 619 13 BU988281 27 45.0 624 12 BG310370	27 45.0 634 9 AV915884 27 45.0 634 10 AV8233455 27 45.0 673 10 AV8233455	27 45.0 661 10 AMZZ3436 27 45.0 954 13 BX329715 26.8 44.7 273 12 BMZ76841	ALIGNMENTS	CE051225 CE051225 LOCUS CE051225 EDEFINITION tigr-gas-dog-17000358147266 Dog Library Canis familiaris genomic,	ACCESSION CE051225 GIS5093664	oss. Canis familiaris Canis familiaris Eukaryota, Metazoa, Chordata, Craniata, V	, Canl	Rusch, D.B., Delcher, A.L., Pop, M., Wang, W. Venter, J.C. The dog genome: survey sequencing and control of the dog genome survey sequencing and control of the dog genome survey.	2 Z Z	COMMENT Contact: Kirkness EF The Institute for Genomic Research Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,	
GenCore version 5.1.6	, using sw model	Run on: June 2, 2004, 18:15:21 ; Search time 1499.5 Seconds (without alignments) 1194.886 Million cell updates/sec	Title: US-10-069-056-11 Perfect score: 60 Sequence: 1 attgctggttttaaacagctgttttatttcatggacca 60	Scoring table: IDENTITY NUC Gapext 1.0	Searched: 27513289 seqs, 14931090276 residues	Total number of hits satisfying chosen parameters: 55026578	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 00% Maximum Match 100% Listing first 45 summaries	Database : EST:* 1: em_estba:* 2. em_esthum.*	2: em_estin:* 4: em_estin:* 5: em_estin:*		8: em_nc:* 9: gb_est1:* 10: gb_est2:*	gb_est3:* gb_est4:* gb_est5:*	17: em_gss_hum:* 18: em_gss_inv:* 19: em_gss_pln:* 20: em_gss_vrt:*			28: gb_gssl:* 29: gb_gss2:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	\$ SUMMARIES	Result Query No. Score Match Length DB ID Description	1 30.4 50.7 661 29 CE051225 CE051225 tigr-gss- C 2 29.2 48.7 414 28 AQ101675 AQ101675 HS 3014 A 3 28.4 47.3 646 28 AZ445628 AZ445628 IMÖZ41106 C 4 28.2 47.0 509 14 CD731301 CD731301 4040794 1

GSS 04-OCT-2000

Location/Qualifiers

FEATURES

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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gellectrophoresis. Vector DNA was prepared from a derivative of pm/1472114[pb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                        AZ445628 646 bp DNA linear GSS 04-OCT-200
1M0241106R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0241106 R, genomic survey sequence.
                                                                                                                                                                                                                                                   Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 646)
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/clone lib="Mouse lokb plasmid UUGCIM library"
/note="Twetcor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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47.3%; Score 28.4; DB 28; Length 646;
Best Local Similarity 70.4%; Pred. No. 2.6e+02;
Matches 38; Conservative 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Erate: 0241 row: I Column: 06
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                               AZ445628.1 GI:10595638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ101675
HS 3014 Al_C10 T7 CIT Approved Human Genomic Sperm Library D Homo
saplens genomic clone Plate=3014 Col=19 Row=E, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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                                                                                                                                                                                                                                                                                                                                             Gaps
                       /organism="Canis familiaris"
/mol type="genomic DNA"
/strain="Standard Poodle"
/db xref="taxon:9615"
/clon= lib="Dog Library"
/note="Site 1: BskXI; Libraries were prepared from peripheral Dlood"
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                                                                                                                                                                                                                                                                                      Length 661;
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High Throughput Sequencing Center
University of Mashington
Tal: (206) 616-3618
Fmax: (206) 616-3818
Fmax: (206) 616-3818
Fmax: (206) 616-3818
Fmax: (206) 616-3818
                                                                                                                                                                                                                                                                                                                                                                                                  3 TTGCTGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATT
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'roganism="Homo sapiens"

/mol type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=3014 Col=19 Row=E"
                                                                                                                                                                                                                                                                                   Query Match 50.7%; Score 30.4; DB 29; Best Local Similarity 77.1%; Pred. No. 68; Matches 37; Conservative 0; Mismatches 11;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="RH03914"
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BU397481.1 GI:25766537
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                                                                                                                                                                                       Rubin, G.M.
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                                                                       CD731301 509 bp mRNA linear EST 26-JUN-2003 4040794 1GAL - Chicken Intestinal Lymphocyte Gallus gallus cDNA clone 1GAL_53G04 5', mRNA sequence.
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Email: hlilleho@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Eases called
by cross match using options -trim_alt '' -trim_fasta. Vector identified
by cross match using options -minmatch 12 -minscore 12
Plate: 53 row: G column: 04
Seq primer: ATTTAGGTGACACTATAG
High quality sequence stop: 509.
1. 509
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                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallue.

1 (bases 1 to 509)

Min,W., Lillehoj,H.S., Ashwell,C.M., Matukumalli,L.K., van Trassel,C. and Han,J.Y.

Chicken intestinal lymphocyte EST database as a resource for the analysis of mucosal immune function
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="lGAL - Chicken Intestinal Lymphocyte"
/note="Organ: Intestine; Vector: pCMV-SPORT6; Site 1:
Sall; Site 2: Not1; Normalized library from chicken gut
infected with coccidia duodenum and middle gut."
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                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Hyun S. Lillehoj
Animal Parasite Diseases Laboratory
Animal and Natural Resources Institute, USDA
Bldg.1043, BARC-East, Beltsville, MD 20705, USA
Tel: 3015048771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="white leghorn SC"
/db_xref="taxon:9031"
/clone="1GAL_53G04"
/sex="mixed"
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Drosophila melanogaster
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/cell_type="Lymphocyte"
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Gallus gallus
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Matches 36; Conservative
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1 (bases 1 to 538).

Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W. T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken CDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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603536587F1 CSEQCHN58 Gallus gallus cDNA clone ChEST499m21 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
Neoptera, Endopterygota, Diptera, Enchycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

1 (Bases I to 536)

2 (Bases I to 536)

2 (Bases I to 536)

3 (Carlson, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., George, R., Guarin, H., Tyler, U., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liso, G., Pholana, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Pholananavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (chicken)
Gallus gallus
Busaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inote="Organ: head; Vector: pFlc1; Site_1: Xho1; Site_2: BamHI, Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male and female"
/dev stage="Adult"
/lab_host="DH5-alpha TonA"
/clone lib="RH Drosophila melanogaster normalized Head
pFlc-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lawrence Berkeley National Lab
Cone Cyclotron Rd, Berkeley, CA 94720, USA
Pax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003603: arm:3R [972216,1267129]
hit genomic AE003803: arm:3R [972216,1267129]
Plate: RH.39 row: B column: 2
High quality sequence stop: 440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 TGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 73.5%; Pred. No. 3.1e+02;
Matches 36; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .536
/organism="Drosophila melanogaster"
/mol type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                     BDGP/HHMI RH Drosophila EST Project Unpublished (2001)
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us-10-069-056-11.rst

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/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: AGGAAACAGCTATGACGAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 102 row: G column: 21
Seg primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  BE722343.1 GI:10123639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Smith TPL
                                                                                        39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (cow)
Bos taurus
                                                Query Match
Best Local Similarity
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BE722343/c
LOCUS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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PUBMED
COMMENT
                                                                                          Matches
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      ORIGIN
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                                                                                                                                                                                  g
                                                                                                                                                                           /dev stage="adult"
//dev stage="adult"
//dev stage="adult"
//dev stage="bt108"
//clone_lib="CSEQCHNS8"
//clone_lib="CSEQCHNS8"
//clone_lib="CSEQCHNS8"
//clone_lib="CSEQCHNS8"
//site_l: EcoRI; Site_2: Not1; This normalized
KS(+); Site_l: EcoRI; Site_2: Not1; This normalized
KS(+); Site_l: EcoRI; Site_2: Not1; This normalized
CDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
vasing methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI; size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kirkness BF
The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CE021004 1300322038797 Dog Library Canis familiaris genomic,
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Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria, Carnivora; Fissipedia; Canidae; Canis.
I (bases 1 to 595)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
47.0%; Score 28.2; DB 13; Length 538;
Best Local Similarity 73.5%; Pred. No. 3.1e+02;
Matches 36; Conservative 0; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 TGTTTTAAACAAGAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'organism="Canis familiaris"
                                                       /organism="Gallus gallus"
/organism="Gallus gallus"
/srzain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST499m21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
Email: Simon. Hubbard@umist.ac.uk.
Location/Qualifiers
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Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic survey sequence.
CE021004
CE021004.1 GI:3503318
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KEYWORDS
SOURCE
ORGANISM
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LOCUS
DEFINITION
                                                  source
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                              FEATURES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

En (bases 1 to 446)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle denome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from day 20 and day 40
embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATTIGCTGTGTTTTAAACACACACAGGGCAAAGAAATGCTGTTTTATTTCATGGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                           1 ATTIGCTGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGA 57
                                                                                                                                                                                               Gaps
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                               ö
                                                                                                                                         Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                          BE722343
190538 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
46.7%; Score 28; DB 10; Length 44
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 40; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VODA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4366 Exa: 402 762 4390 Email: smith@email.marc.usda.gov
                                                                                                                                            47.0%; Score 28.2; DB 29;
68.4%; Pred. No. 3e+02;
Live 0; Mismatches 18;
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 35; Conserv
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 PUBMED
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KEYWORDS
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                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ427038 518 bp mRNA linear EST 01-SEP-2002 CGHem 027-A-16 C. gigas Hemocytes Lambda Zap Express Library Crassostrea gigas CDNA, mRNA sequence.
                                                                                                                                     Crassostrea gigas (Pacific oyster)

Crassostrea gigas

Crassostrea gigas

Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Ostreoida;

Ostreoidae; Ostreidae; Crassostrea.

(bases 1 to 518)

Gueguen,Y., Cadoret,J.P., Flament,D., Barreau-Roumiguiere,C.,

Immune gene discovery by expressed sequence tags generated from hemocytes of bacteria-challenged oyster, Crassostrea gigas

Contact: Escoubas J.M. Bachere E.

Defences et Resistances chez les Invertebres Marins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 28-NOV-2000
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DRIM, CNRS-IFREMER, CC80, 2 Place E. Bataillon, Montpellier 34095,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATTTGCTGTGTTTTAAACAGACGAGGCAAAAGAAATGCTGTTTTATTTCATGGACCA 60
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF401923
UI-R-CA1-bil-c-02-0-UI.sl UI-R-CA1 Rattus norvegicus cDNA clone
UI-R-CA1-bil-c-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.7%; Score 28; DB 13; Length 518; 66.7%; Pred. No. 3.6e+02; ive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: jmescoub@ifremer.fr; ebachere@ifremer.fr
Seq primer: T3 primer: aattaaccctcactaaaggg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Crassostrea gigas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:29159"
/cell_type="hemocytes"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF401923.1 GI:11389898
                                                                                                        BQ427038.1 GI:22598623
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                                                                                                                                                                                                                                                                                                                                                                                                            Tel: (0) 467144625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 66.7
Matches 40; Conservative
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BQ427038
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University of Iowa 135 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA 7e1: 319 335 8250
Fax: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@ulowa.edu
The sequence contained an Oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized hypothalamus library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Seg primer: M13 Forward
POLYA-Yes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10116".
/clone="ULR-CA1-bil-c-02-0-UI"
/lab_host="DH10B [fife Technologies)"
/clone lib="ULR-CA1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note:"vector: pt7T3D-Pac (Pharmacia) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA710811 402 bp mRNA linear EST 24-DEC-1997 vt93d02.rl Soares mammary gland NbMMG Mus musculus cDNA clone IMAGE:1178691 5', mRNA sequence.
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Mus musculus
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata, Sciurognathi; Muridae; Murinae;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba-T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Morre, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
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ilarity 74.5%; Pred. No. 4.6e+02;
Conservative 0; Mismatches 12;
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/strain="Sprague-Dawley"
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TAG_LIB=UI-R-CA1
TAG_SEQ-GATGC"
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The WashU-HHMI Mouse EST Project
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MGI:506832
MGI:697405
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AA509795/c
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Mus musculus
Mus mecaca, Chordata, Craniata, Vertebrata, Euteleostomi;
Bukaryota, Metazoa, Chordata, Sciurognathi; Muridae, Murinae, Mus
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 455)
Marra, M. Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marra, M., Hallier, L., Allen, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
WashIngton University School of Medicinep
Fal: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: and 2886 1810
Fax: branch and a season a 
                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available.royalty.free through LLNL ; contact the
This clone is available.royalty.free through LLNL ; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
MGI:636539
Seg primer: -28m13 rev2 ET from Amersham
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   Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 4.3e+02;
0; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 395.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:1178691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="C57BL/6J"
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Best Local Similarity 69.1%;
Matches 38; Conservative 0
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AA981917/c
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryota, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 468) Marra, Murita, Musia, Murita, Musia, Mu
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vg29a09.rl Soares mammary_gland_NbWMG Mus musculus cDNA clone
lMAGE:862744 5', mRNA sequence.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
Unpublished (1996)
Contact: Marxa M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
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High quality sequence stop: 381.
Location/Qualifiers
Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 448.
Location/Qualifiers
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="male"
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Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                               /dev stage="bullow" unaminary gland NbbWG"
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/lab_host="DH10B"
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/note="Gran: mammary gland; VecTor: pt not I;
/note="Gran: mammary gland; VecTor: pt note"
/note="Gran: mammary gland; VecTor: pt note; Ve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="660" - Mixed stages of anther and pollen" /clone="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI; Site_2: KhoI; Anther and pollen cDNA library.
Directionally sequenced with 5' end at the EcoRI site.
Created by Amie Franklin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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/tissue type="whole premieotic anthers to pollen shed"
/dev_stage="premieotic anthers to pollen shed"
/lab_host="XLOLR"
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Pred. No. 4.2e+02;
0; Mismatches 17; Indels (
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855 California Ave, Palo Alto, CA 94304, USA
TTE1: 650 723 2237
Fax: 650 725 8221
                                                                                                                                                type="mammary gland"
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Department of Biological Sciences
                                               /db_xref="taxon:10090"
/clone="IMAGE:862744"
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/cultivar="Ohio43"
          /strain="C57BL/6J"
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AW499334
AW499334.1 GI:7137911
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Walbot, V.
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Unpublished (1999)
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46.3%; Score 27.8; DB 10; Length 541;

Query Match

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/organism="Zea mays"
/wol type="mRNA"
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/note="Organ: Kernel; Vector: pAb-GAL4-2'; Site_l: EcoRI;
Site_2: Xhol; Kernel endosperm cDNA library from Schmidt
                                                                                                                                                                                                        608 bp mRNA linear EST 02-FEB-2000
CDNA, mRNA sequence.
A1665130
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Maize ESTB from various cDNA libraries sequenced at Stanford
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                                                                      3 TIGCIGIGITITIAAACAGACAAGGAGCAAAAGAAATGCIGITITITITICAIGGA
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Pred. No. 4.1e+02;
0; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Biological Sciences
Stanford University
Scalifornia Ave, Palo Alto, CA 94304, US
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbocestenford.edu
Plate: 605007 row: B column: 08.
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Job time : 1505.5 secs
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  L Similarity 69.1%;
38; Conservative
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Unpublished (1999)
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Zea mays
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Sequence 1 Sequence 2 Sequence 3 Sequence 5 Sequence 5

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Sequence 19, Sequence 531

Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2

US-09-540-236-177 US-09-596-002-30 US-09-245-01-5 US-09-679-409-1 US-09-007-119-8 US-09-109-476-242 US-09-149-476-242 US-09-149-476-242 US-09-149-476-241 US-09-149-476-241

Sequence 7, Appli Sequence 131, App Sequence 3, Appli

Sequence

US-09-673-395A-19 US-09-673-395A-531 US-09-731-166-7 US-09-325-932A-131 US-09-245-041-3

ALIGNMENTS

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38.0 1001
38.0 1419
38.0 1419
38.0 39609
38.0 319608
37.7 1286
37.7 2624
37.7 2624
37.7 2624
37.7 3687
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Sequence 55, Appl
Sequence 35, Appl
Sequence 3956, Ap
Sequence 1178, Ap
Sequence 1178, Ap
Sequence 1105, Ap
Sequence 1, Appli
Sequence 286, Ap
Sequence 286, Ap
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Sequence 2551, Ap
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Sequence 1, Appli
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Sequence 54
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*

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(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-336-345-2
US-08-647-655-1
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US-09-702-705-1581
US-09-736-457-1581
US-09-614-124B-1581
US-09-671-325-1581
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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No.
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Pred. No. 1.7e-05;
0; Mismatches 7; Indels 0
                                                                    APPLICANT: Parxish, Colin R.
APPLICANT: Gruenberg, Allen
APPLICANT: Gruenchael, Leland E.
APPLICANT: Carmichael, Leland E.
NITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 CARDERSEER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
STREET: 1155 Avenue of the Americas
STATE: New York
STATE: NW
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYEE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAETENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30753
REFERENCE/DOCKET NUMBER: 30753
REPERENCE/DOCKET NUMBER: 30753
REFERENCE/DOCKET NUMBER: 30753
TELECHONE: (212) 790-9090
TELEFAX: (212) 790-9090
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 5049 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
Sequence 1, Application US/08336345
Patent No. 5814510
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.3%;
87.0%;
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 87.08
Matches 47; Conservative
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ORGANISM: Parvovirus
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7 IGIGITITIAAACAGACAAAGGAAGCAAAAGAAAIGCIGITITIAITITCAIGGACCA
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Sequence 1, Application US/08647655

Patent No. 588585

GENERAL INFORMATION:
APPLICANT: Carmichael, Colin R.
APPLICANT: Carmichael, Leland E.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEB: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STREET: New York
                                                                                                                                       APPLICANT: Parrish, Colin R.
APPLICANT: Gruenberg, Allen
APPLICANT: Gramichael, Leland E.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCE: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.3%; Score 42.8; DB 1; Length 5049; Best Local Similarity 87.0%; Pred. No. 1.7e-05; Indels 0; Matches 47; Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/336,345

FILING DATE:

CLASSIFICATION: 424

ATTOMNEY/AGENT INFORMATION:

NAME: Gordon, Jennifer

REGISTRATION NUMBER: 30753

REGISTRATION NUMBER: 3793-006

TELECOMMUNICATION INFORMATION:

TELEFRORE (212) 790-9090

TELEFRA: (212) 790-9090

TELEFRA: (212) 790-9090

TELEFRA: (212) 790-9066

TELEFRA: (212) 809-8064/9741

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTER ESTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIRE: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                 Sequence 2, Application US/08336345
Patent No. S814510
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 5049 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE:
CORGANISM: Parvovirus
US-08-336-345-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-647-655-1
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APPLICANT: Built et al.

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococc Patent No. 6503729

TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1995-08-22
                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                DB 4; Length 580073;
                                                                                                                                                                                                                                               1 ATTTGCTGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCA
                                                                                                             Score 25:8; DB 4; Length 5
Pred. No. 27;
0; Mismatches 17; Indels
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OTHER INFORMATION: n equals a, t, c, or g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08916421B Patent No. 6503729 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Methanococcus jannaschii
, ORGANISM: Mycoplasma genitalium
US-08-545-528D-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COCATION: (28222)...(28222)
OTHER INFORMATION: n equals a,
NAME/KEY: misc. feature.
LOCATION: (28257)...(28258)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COCATION: (98239)..(98239)
THER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a,
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LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a,
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LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a,
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                                                                                                             Query Match
Best Local Similarity 67.9%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
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LOCATION: (98120)..(98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
LENGTH: 1664976
                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-08-916-421B-1
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TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment Patent No. 6537773

TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: P8193P1

CURRENT APPLICATION WUMBER: US/08/545,528D

CURRENT FILING DATE: 1995-10-19
PRIOR PILING DATE: 1995-06-07
PRIOR PILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin version 3.1
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Pacent No. 6476212

GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PERL Program
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                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700349086H1
US-09-313-294A-4824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26.8; DB 4;
Pred. No. 2.3;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                       Score 42.8; DB 2;
Pred. No. 1.7e-05;
0; Mismatches 7;
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US-08-545-528D-1
'S-08-545-528D-1
'Sequence 1, Application US/08545528D
'Patent No. 6537773
'GENERAL INFORMATION:
                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                          71.3%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 68.5%;
Matches 37; Conservative
   LENGTH: 5049 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 87.0
Matches 47; Conservative
                                                                                                                                                                                                         ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .09-313-294A-4824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
LENGTH: 580073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4824
LENGTH: 277
                                                                                                                                                                                                                                                                                                         US-08-647-655-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         요
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c, or g ö ö or or or or ö or ö or ö ö or VAME/KEY: misc feature CCATION: (622708)..(622708) OTHER INFORMATION: n equals a, t, C, VAME/KEY: misc\_feature LOCATION: (657081)..(657081) DIHER INFORMATION: n equals a, t, C, AME/KEY: misc feature LOCATION: (312837) .. (312837) THER INFORMATION: n equals a, t, C, ϋ OTHER INFORMATION: In equals a, t, c, corrections (657203)...(657203)...(657203)...(657203)...(657203)...(657203)...(657203)...(657203)...(657203)...(657203)...(67435)...(674435)...(674435)...(674435)...(674435)...(674435)...(674435)...(674435)...(674420)...(682442)...(68244 LOCATION: (234814)...(234814)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misec\_feature
LOCATION: (303598)..(309398)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misec\_feature
LOCATION: (309418)
OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc\_feature
LOCATION: (319226). (319226)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc\_feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t, c,
MAME/KEY: misc\_feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc\_feature
LOCATION: (659924)..(600992)
OTHER INFORMATION: n equals a, t, c,
OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc\_feature LOCATION: (779676).(779676) OTHER INFORMATION: n equals a, t, NAMEKEY: misc\_feature LOCATION: (855539).(855539) WANE/KEY: misc feature LOCATION: (231980)..(231980) OTHER INFORMATION: n equals a, t, OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (871619)..(871619) NAME/KEY: misc feature LOCATION: (234187)..(234187) OTHER INFORMATION: n equals a, t, LOCATION: (779455)..(779455) OTHER INFORMATION: n equals a, t, LOCATION: (191989)..(191989) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (234220)..(234220) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (234814)..(234814) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature\_ LOCATION: (312993)..(312993) OTHER INFORMATION: n equals a, t, COCATION: (191995)..(191995) THER INFORMATION: n equals a,

Query Match 42.3%; Score 25.4; DB 4; Length 1664976; Best Local Similarity 74.4%; Pred. No. 43; Matches 32; Conservative 0; Mismatches 11; Indels 0; LOCATION: (1664854)...(1664855)
COTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1 b ö or ö c, or or οr ör ö ö ö 9 NAME/KEY: misc feature LOCATION: (1470091)..(1470091) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (1084830). (1084830) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (1096846)..(1096846) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (1119881)..(1119881) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (1130881). (1130881)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1349473)..(1349491)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (13499491)..(1349491) NAME/KEY: misc feature
LOCATION: (1569020). (1569020)
OTHER INPORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1602912).. (1602912)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1603734).. (1603734)
OTHER INFORMATION: n equals a, t NAME/KEY: misc feature LOCATION: (1637998)..(1637998) OTHER INFORMATION: n equals a, INFORMATION: n equals a,

315581 AATCAGAAAAGGCAATAAAAAATATGCTGTTTTATTTAAAGAA 315623 15 AAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGA 57 셤 à

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0; Gaps

Sequence 1, Application US/09790988

| Sequence 1, Application US/09790988
| Patent No. 6632935
| GENERAL INFORMATION:
| APPLICANT: SHIGENOBU, SHUJI
| APPLICANT: WATANABE, HIDEM
| APPLICANT: MATANABE, HIDEM
| APPLICANT: BAKAKI, YOSHIVUKI
| TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
| TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
| CURRENT APPLICATION NUMBER: US/09/790,988
| CURRENT APPLICATION NUMBER: J001-02-23
| PRIOR FILING DATE: 2000-04-07
| WHEN FILING DATE: 2000-04-07
| WHEN FILING DATE: 2000-04-07
| SEQ ID NO 1
| LENGTH: 640681 RESULT 8 US-09-790-988-1

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APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENCTH: 46899 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                              USA
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HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-998-416-54/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN:
US-08-471-119A-1
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta

APPLICANT: Bougueleret, Lydie

APPLICANT: Chumakov, Ilya

APPLICANT: Chohen, Annick

TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING

TITLE OF INVENTION: GENSEI NVOLVED IN ARACHIDONIC ACID METABOLISM

TILE REFERENCE: GENSEI 051CP1

TILE REFERENCE: GENSEI 050C-08-16

CURRENT APPLICANTON NUMBER: US 60/133,200

PRIOR APPLICANTON NUMBER: US 60/133,200

PRIOR FILING DATE: 1999-03-21

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-21

NUMBER OF SEO ID NOS: 1304

SEOFWARE: Patent.pm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATTIGCTGTGTTTTAAACAGACAGAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGAC 58
                                                                                                                                                                                                                        292498 TGTTTATTACGTATAAAATGGCGCAAAAAAATGCAGTGTTATTTAAGG 292546
                                                                                                                                                ö
                                                                                         Score 25; DB 4; Length 640681;
Pred. No. 50;
0; Mismatches 15; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.7%; Score 24.4; DB 4; Length 1001; illarity 63.8%; Pred. No. 20; Conservative 0; Mismatches 21; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 756..775
OTHER INFORMATION: upstream amplification primer, complement NAME/KEY: primer bind
LOCATION: 288..307
OTHER INFORMATION: downstream amplification primer
NAME/KEY: misc_binding
LOCATION: 489..513
OTHER INFORMATION: 12-113-276 potential probe
                                                                                                                                                                                             7 TGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_binding
LOCATION: 502.521
LOCATION: 12-113-276.misl, potential complement
NAME/KEY: misc_binding
LOCATION: 482.500
OTHER INFORMATION: 12-113-276.mis2
NAME/KEY: primer_bind
LOCATION: 786.775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 501
OTHER INFORMATION: 12-113-276 : polymorphic base T or C
                                                                                                                                                                                                                                                                                                                                                         ## Sequence 310, Application US/09641638 | Patent No. 6432648 | Patent No. FORWATION: APPLICANT: Blumenfeld, Marta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: 994 -
; OTHER INFORMATION: n=a, g, c or t
US-09-641-638-310
                                                                                            41.7%;
                                                                                         Query Match
Best Local Similarity 69.4<sup>1</sup>
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 37; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,119A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100-8029/CONT/CONT
                                                                           APPLICANT: Lettner, Ernst
APPLICANT: Schneider, Elisabeth
APPLICANT: Schneider, Elisabeth
APPLICANT: Schneider, Elisabeth
APPLICANT: Schneider, Elisabeth
APPLICANT: Schneider, Kurt
APPLICANT: Weber, Gerhard
TITLE OF INVENTION: Cyclosporin Synthetase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5927706artis Corporation
STREET: 59 Route 10
CITY: Bast Hanover
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Match 40.7%; Score 24.4; D
Local Similarity 63.8%; Pred. No. 46;
les 37; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 54, Application US/08998416 Patent No. 6239264 GENERAL INFORMATION:
Sequence 1, Application US/08471119A
Patent No. 5827706
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Tolypocladium niveum
ATCC 34921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 100-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8474
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
```

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APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIM, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 icracididaricakagagdargagdaarraracaaridcaciriricaridak 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 TGTGTTTTAAACAGACGAGGGGAAAAGAAATGCTGTTTTATTTCATGGA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
39.7%; Score 23.8; DB 4; Length 8537;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 34; Conservative 0; Mismatches 17; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24; DB 3; Length 716;
Pred. No. 25;
0; Mismatches 20; Indels
                                                      FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/ARENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 919-541-8689
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TTTGCTGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR PPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
LENGTH: 8537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42, Application US/10204708
Patent No. 6677731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 64.3%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 716 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                   24-DEC-1997
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: PAG1015UP
US-08-998-416-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
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                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/97
FILING DATE: 31-DEC-1996
ATTONNEY/AGENT INPORMATION:
NAME: MAGISH J. Timothy
REGISTRATION NUMBER: PP/5-30306/A/CGC1976
TELEPHONE: 919-541-8689
INFORMATION ED SEQUENCE CHARACTERISTICS:
CLEBRANT SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
CITY: Rosearch Triangle Park
COUNTRY: USA
                       ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
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APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENONIC DNA SEQU
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATEIDE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                          ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Pohlmann, Rainer
Steiner, Sabine
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Best Local Similarity 64.3
Matches 36; Conservative
                    CORRESPONDENCE ADDRESS:
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GENERAL INFORMATION:
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Sequence 3955, Application US/09328352

Releant No. 6562958

GRNERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRESENCE: Gr29-0328
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 3956
LENGTH: 1335
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ITLE OF INVENTION: No. 6569662el Nucleic Acids and
ITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                               Score 23.6; DB; Pred. No. 39; 0; Mismatches
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; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: PLE_Genes Version 1.0
; SEQ ID NO 567
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Patent No. 6569662
                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3956
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 69.6%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
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Wehrman, Tom
Xue, Aidong J.
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Wang, Dunrui
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; LOCATION: (1)..(1386)
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Search completed: June 3, 2004, 00:56:26 Job time: 38.75 secs

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The present sequence is a peptide fragment of parvovirus non-structure protein 1 (NS1) variant (T394A). The invention relates to the variants the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytocoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parvovirus non-structure protein 1 (NS1) variant (T394A) peptide.
/note= "Wild type Thr substituted with Ala"
                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                   AAE28646
AAE28647
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ABU64867
ABU64762
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AAE26944
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ABU64764
ABR43402
AAY97723
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AAE26942
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N-PSDB; AAD02802.
 Misc-difference
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Aay72706 Parvoviru
Aay72702 Parvoviru
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              GenCore version 5.1.6
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Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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/note= "Wild type Thr substituted with Ala"
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                             AAY72710 standard; protein; 672 AA
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31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is parvovirus non-structure protein 1 (NS1) variant (T394A). The invention relates to the variants of the parvovirus nonstructure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as toxins for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                             NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild type Thr substituted with Ala"
                                           Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                    Indels
                                                                                                                                                                                                                                                       Parvovirus non-structure protein 1 (NS1) variant (T394A)
on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 113; DB 4;
Pred. No. 1.1e-08;
; Mismatches 0;
                                             100.0%; Score 113; DB 4; 100.0%; Pred. No. 2.7e-10;
                                                                    ö
                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 25-27; 41pp; English.
                                                                                                                                                                           AAY72708 standard; protein; 672 AA.
                                                                                                       1 ICCVLNRQGGKRNAVLFHGP 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
ilarity 100.0%;
Conservative 0;
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                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nueesch J, Rommelaere J;
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-212717/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 20; Conserv
                                                         Best Local Similarity Matches 20; Conserv
  (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD02803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 672 AA;
                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                         Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                  EP1077260-A1
                                                                                                                                                                                                                          06-AUG-2003
31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-2001
                                                                                                                                                                                                                                                                                                                     Parvovirus
                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                 AAY72708;
                                                 Query Match
    therapy.
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                    The present sequence is partorning non-
(1463A). The invention relates to the variants of the parvovirus non-
structure protein (NSI) having a shifted equilibrium between the DNA
replication and transcription activities, and the cytotoxicity activity.
These variants are useful as toxins for treating tumoural diseases. The
variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
                                                                                                                                                                                                                                                                 Gaps
sequence is parvovirus non-structure protein 1 (NS1)
                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                        Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parvovirus non-structure protein 1 (NS1) variant (T363A).
                                                                                                                                                                                                                                                                    Indels
                                                                                                            variant DNAs are useful as vectors for gene therapy.
2003 to correct OS field.)
                                                                                                                                                                                                                        96.5%; Score 109; DB 4;
95.0%; Pred. No. 4.4e-08;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY72706 standard; protein; 672 AA.
                                                                                                                                                                                                                                                                                                                                             1 ICCVLNRQGGKRNAVLFHGP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
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                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 19; Conserv
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31-MAY-2001
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ID AAY7
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AC AAY7
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DT 06-P
DT 31-N
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The present sequence is a parvovirus wild-type non-structure protein 1 (NS1). The present invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                               Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild type Ser substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parvovirus non-structure protein 1 (NS1) variant (S283A).
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                 DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY72704 standard, protein, 672 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             381 ICCVLNROGGKRNTVLFHGP 400
                                                                                                                                                                      Disclosure; Fig 1; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 1 ICCVLNROGGKRNAVLFHGP 20
                                                                                                                                                                                                                                                                                                                                          Query Match 96.5%;
Best Local Similarity 95.0%;
Matches 19; Conservative
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(first entry)
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                                             Rommelaere
                                                                      WPI; 2001-212717/22.
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                                                                                   N-PSDB; AAD02797
                                                                                                                                                                                                                                                                                                               Sequence 672 AA;
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31-MAY-2001
                                             Nueesch J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is parvovirus non-structure protein 1 (NS1) variant (T363A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                     Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
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                                                                                                             /note= "Wild type Thr substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.5%; Score 109; DB 4; Length 672; 95.0%; Pred. No. 4.4e-08; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parvovirus wild-type non-structure protein 1 (NS1).
                                                                           .... Location/Qualifiers Misc-difference 363
                                                                                                                                                                                                                                                         (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 19-21; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY72702 standard; protein; 672 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ICCVLNRQGGKRNAVLFHGP 20
                                                                                                                                                                                                  99EP-00115161.
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                                                                                                                                                                                                                                                                                     Nueesch J, Rommelaere J;
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                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD02801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 672 AA;
                                                                                                                                          EP1077260-A1
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                                           Parvovirus
                                                          Synthetic
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AAY7270
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Gaps

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Score 109; DB 4; Length 672; Pred. No. 4.4e-08; 0; Mismatches 1; Indels

3

Gaps

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Indels

4;

2; Mismatches

1 ICCVL----NRQG-GKRNAVLFH 18

3 ICCAAVNCSNRQGKGEKRAVSFH

25

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(first entry)

Length 90;

Score 49.5; DB 7; Pred. No. 7.4;

43.8%;

Conservative

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This invention relates to a method of identifying a compound which modulates THAP (THANCOS (death) Associated Protein)-mediated activities. The invention also relates to genes and proteins of the THAP family and uses thereof. Coordination of cell proliferation and cell death is required for normal development and tissue homeostasis in multicellular organisms. A defect in these two processes is a fundamental requirement for tumourigenesis. THAP1 is a pro-apoptotic protein and therapeutics which modulate THAP1 activity may be cytostatic. The sequences of the invention may prove useful for gene therapy. The method is useful for preparing a composition for treating cancer. The present sequence is the partial amino acid sequence of the human THAP4 protein which was used for homology purposes in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Girard J, Roussigne M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-532998/50.
                                                                                                                                               Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003051917-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 90 AA;
                                                                                                                Sequence 672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                   15-JAN-2004
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                                                                                                                                                                                                                                                                                            ADD36322;
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 THAP4.
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Matches
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8X222222228
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Kossida S, Amalric F;

SAS.

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THAP; THantos (death) Associated Protein; THAP family; cell proliferation; cell death; tissue homeostasis; tumourigenesis; THAPI; pro-apoptotic protein; cytostatic; gene therapy; cancer; mouse;
                                                                                                                                                                                                                                                                                   Mouse orthologue to human THAP (THantos Associated Protein) Seq ID25.
                                                                                                                                                                                            ADD36217 standard; protein; 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CNRS ) CNRS CENT NAT RECH SCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-2001; 2001US-0341997P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Girard J, Roussigne M,
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-532998/50.
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                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus.
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                                                                                                                                                                                                                              ADD36217;
                                                                                                                                                                                                                                                                                                                                                                             murine.
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                                                                                                                                                               RESULT
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                                  The present sequence is parvovirus non-structure protein 1 (NSI) variant (S283A). The invention relates to the variants of the parvovirus non-structure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THAP; THantos (death) Associated Protein; THAP family; cell proliferation; cell death; tissue homeostasis; tumourigenesis; THAPI; human; pro-apoptotic protein; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a test compound that modulates THAP-mediated activities f
treating cancer by determining whether the test compound selectively
modulates the activity of the THAP-family polypeptide.
                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                 Score 109; DB 4; Length 672;
Pred. No. 4.4e-08;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                     0; Mismatches
          Claim 6; Page 14-16; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    ADD36322 standard; protein; 90 AA
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                                                                                                                                                                                                                                                                     1 ICCVLNRQGGKRNAVLFHGP 20
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(CNRS ) CNRS CENT NAT RECH SCI
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                                                                                                                                                                                                       96.5%;
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7
                                                                                                                                                                     This invention relates to a method of identifying a compound which modulates THAP (THantos (death) Associated Protein)-mediated activities. The invention also relates to genes and proteins of the THAP family and uses thereof. Coordination of cell proliferation and cell death is required for normal development and tissue homeostasis in multicellular organisms. A defect in these two processes is a fundamental requirement for tumourigenesis. THAP1 is a pro-apoptotic protein and therapeutics which modulate THAP1 activity may be cytostatic. The sequences of the invention may prove useful for gene therapy. The method is useful for penaltial a composition for treating cancer. The present sequence is the amino acid sequence of mouse orthologue of the human THAP proteins which is related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Identifying a test compound that modulates THAP-mediated activities f
treating cancer by determining whether the test compound selectively
modulates the activity of the THAP-family polypeptide.
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Pred. No. 7.
                                                                                                                                 Claim 16; SEQ ID NO 25; 303pp; English.
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52.2%;
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Matches 12, Conservative
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antiinflammatory; thyromimetic; antiallergic; cerebroprotective;
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ABR58511
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                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a method of identifying a compound which modulates THAP (THantos (death) Associated Protein)-mediated activities. The invention also relates to genes and proteins of the THAP family and uses thereof. Coordination of cell proliferation and cell death is required for normal development and tissue homeostasis in multicellular organisms. A defect in these two processes is a fundamental requirement for tumourigenesis. THAP1 is a pro-apoptotic protein and therapeutics which modulate THAP2 activity may be cytostatic. The sequences of the invention may prove useful for gene therapy. The method is useful for amino acid sequence of a mouse orthologue of the human THAP proteins which is related to the invention.
                                                                                                                                                                                                                                                                                                                                                     Identifying a test compound that modulates THAP-mediated activities for treating cancer by determining whether the test compound selectively modulates the activity of the THAP-family polypeptide.
                                                                                                THAP; THantos (death) Associated Protein; THAP family; cell proliferation; cell death; tissue homeostasis; tumourigenesis; THAPI; pro-apoptotic protein; cytostatic; gene therapy; cancer; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; SECP; neuroprotective; relaxant; antithyroid;
antidiabetic; cytostatic; dermatological; immunosuppressive;
                                                                            Mouse orthologue to human THAP (THantos Associated Protein) Seq ID102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein Incyte ID No: 7504539CD1 SEQ ID NO: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.8%; Score 49.5; DB 7; Length 205; 52.2%; Pred. No. 17; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                          Amalric F;
                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; SEQ ID NO 102; 303pp; English.
                                                                                                                                                                                                                                                                                                          Girard J, Roussigne M, Kossida S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ICCVL----NRQG-GKRNAVLFH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD36294 standard; protein; 205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR58515 standard; protein; 548 AA.
                                                                                                                                                                                                                                                                                   CNRS CENT NAT RECH SCI
                                                                                                                                                                                                                            10-DEC-2002; 2002WO-EP014027.
                                                                                                                                                                                                                                                  18-DEC-2001; 2001US-0341997P.
                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
                                                                                                                                                                                                                                                                         (ENDO-) ENDOCUBE SAS
                                                                                                                                                                                                                                                                                                                               WPI; 2003-532998/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 205 AA;
                                                                                                                                                                                WO2003051917-A2.
                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUL-2003
                                                       15-JAN-2004
                                                                                                                                                                                                      26-JUN-2003
                                  ADD36294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR58515;
                                                                                                                                                                                                                                                                                    (CNRS )
                                                                                                                                    murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
ADD36294
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The invention relates to a novel isolated human secreted polypeptide (SECP). An SECP of the invention has neuroprotective, relaxant, antitipated, antidiabetic, cytostatic, dermatological, immunosuppressive, antidialmatory, thyromimetic, antiallergic, cerebroprotective, gastrointestinal, hepatotropic, antiallergic, cerebroprotective, cartioride, uropathic, antibatesatic, imparting protozoacide, virucide, uropathic, antibatesatic, cardiovascular, anti-HIV, and nootropic antiaponist. The polypeptide may act as either a SECP agonist or antagonist. The polypeptide may act as either a SECP agonist or antagonist. The polypeptide may act as either a secP agonist or antagonist. The polypeptide are useful in diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of SECP, such as neurodegenerative disorders, muscular disorders, endocrine disorders, infections, cardiovascular disorders, cardiovascular disorders, cenal disorders, infections, cardiovascular disorders or hepatic. compounds that specifically bind to and modulate the activity of SECP. The polyments may also be used in screening for compounds that specifically bind to and modulate the activity of SECP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
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gastrointestinal; hepatotropic; nephrotropic; anticonvulsant; fungicide; antiparkinsonian; antibacterial; antiparasitic; protozoacide; virucide; uropathic; antirheumatic; cardiant; cardiovascular; anti-HIV; nootropic; gene therapy; neurodegenerative disorder; muscular disorder; cancer; endocrine disorder; immunological disorder; gastrointestinal disorder; renal disorder; infection; cardiovascular disorder; hepatic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New SECP polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of SECP, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lehr-Mason PM, Tran UK, Duggan BM;
J, Xu Y, Tang TY, Chawla NK, Elliott VS;
SD, Yao MG, Emerlian Grifffin JA, Lal PG;
Ghn MR, Lee SY, Ramkumar J, Gorvad AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represent the human SECP's of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J J, Xu Y, Tang Ty
a SD, Yao MG, Emer
aghn MR, Lee EA, I
Borowsky ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 166-168; 192pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ICCVL----NRQG-GKRNAVLFH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-OCT-2001; 2001US-0326945P.
19-OCT-2001; 2001US-034371BP.
02-NOV-2001; 2001US-0343980P.
16-NOV-2001; 2001US-0332426P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2002; 2002WO-US032032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thangavelu K, Yang J, Xu
Forsythe IJ, Becha SD, Y
Zebarjadian Y, Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thangaver.
Forsythe IJ, Becna
Zebarjadian Y, Baugh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-371995/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ACC72453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 548 AA;
                                                                                                                                                                                                                                                                                                                                                                 WO2003029437-A2
                                                                                                                                                                                                                                                                                       Homo sapiens.
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Sequence 577 AA; Query Match Ношо 

Local Similarity ADD36198 6 ଚ g SECP, such as neurodegenerative disorders, muscular disorders, endocrine disorders, endocrine disorders, ancers, immunological disorders, muscular disorders, endocrine fisorders, infections, cardiovascular disorders, or hepatic compounds that specifically bind to and modulate the activity of SECP. The polynucleotides can be used to create humanized animals or transgenic animals to model human disease. The sequences shown in ABR58489-ABR58520 represent the human SECP's of the invention The invention relates to a novel isolated human secreted polypeptide (SECP). An SECP of the invention has neuroprotective, relaxant, antithyroid, antidiabetic, cytosteatic, dermatological, immunosupressive, antinflammatory, thyromimetic, antiallergic, cerebroprotective, gastrointestinal, hepatotropic, nephrotropic, anticonvulsant, antipacterial, antiparsticic, fungicide, protozocide, vircide, uropathic, antirheumatic, cardiant, cardiovascular, anti-HHV, and nootropic activity. A polymotleotide of the invention may have a use in gene therapy, and a polymeptide may act as either a SECP agonist or antagonist. The polypeptide or its fragments, and the polymotleotide encoding the polypeptide are useful in diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of antidiabetic; cyfostatic; dermatological; immunosuppressive; antinflammatory; thyromimetic; antiallergic; cerebroprotective; astinflammatory; thyromimetic; antiallergic; cerebroprotective; antipatoricip; anticonvulsant; fungicide; antipatorian; antibacterial; antiparasitic; protezoacide; virucide; uropathic; antirheumatic; cardiant; cardiovascular; anti-HIV; nootropic; gene therapy; neurodegenerative disorder; muscular disorder; cancer; endocrine disorder; immunological disorder; gastrointestinal disorder; renal disorder; hepatic disease. New SECP polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of SECP, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and secreted protein; SECP; neuroprotective; relaxant; antithyroid; Yue H, Warren BA, Lehr-Mason PM, Tran UK, Duggan BM; Thangavelu K, Yang J, Xu Y, Tang TY, Chawla NK, Elliott VS; Forsythe IJ, Becha SD, Yao MG, Emerling BM, Griffin JA, Lal PG; Zebarjadian Y, Baughn MR, Lee EA, Lee SY, Ramkumar J, Gorvad AE; Human secreted protein Incyte ID No: 7503072CD1 SEQ ID NO: 23. Claim 1; Page 162-163; 192pp; English ABR58511 standard; protein; 577 AA Thangave---Forsythe IJ, Becma Zebarjadian Y, Baughn MR, Lu--03-0CT-2001; 2001US-0326945P. 19-0CT-2001; 2001US-034371BP. 02-NOV-2001; 2001US-0343980P. 16-NOV-2001; 2001US-0332426P. 03-OCT-2002; 2002WO-US032032 (INCY-) INCYTE GENOMICS INC. (first entry) WPI; 2003-371995/35. N-PSDB; ACC72449 WO2003029437-A2. 08-JUL-2003 .0-APR-2003 e.g. neurc infection ABR58511;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activities for
selectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THAP; THantos (death) Associated Protein; THAP family; cell proliferation; cell death; tissue homeostasis; tumourigenesis; THAP1; human; pro-apoptotic protein; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a test compound that modulates THAP-mediated treating cancer by determining whether the test compound modulates the activity of the THAP-family polypeptide.
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human THAP (THantos (death) Associated Protein) 4.
                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Girard J, Roussigne M, Kossida S, Amalric F;
  ed. No. 52;
Mismatches
ilarity 52.2%; Pred. No. Conservative 2; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; SEQ ID NO 6; 303pp; English
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                                                                                       18
                                                                                                                                                                                                                                                                                        ADD36198 standard; protein; 577 AA.
                                                                                       1 ICCVL----NRQG-GKRNAVLFH
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|ICCAAVNCSNRQGKGEKRAVSFH
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N-PSDB; ADD36355, ADD36442.
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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tes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 577 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                       15-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                ADD36198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THAP4.
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RESULT 13 AAW13494

DB 6; Length 577;

43.8%; Score 49.5;

Thu Jun

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chronic constriction injury; CCI; spared nerve injury; SNI; Chung
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                         Rattus norvegicus
                                                                                                                                                                                    (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 298 AA;
                                                                                                                                                                                                                                                GENBANK; S32426.
                                                WO2003016475-A2
                                                                       27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA011564;
                                                                                                                                                                                                            Woolf C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA011564
 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The herpes helper virus (HHV-6) transcription suppressor (ts) gene shuts off transcription of the HIV long terminal repeat promoter and of the H-c ras gene. A new gene therapy method for treating a subject at risk of or suffering from a disease state associated with oncogenic transformation or lentivirus infection comprises delivering a vector comprising a polynucleotide sequence encoding a transcription suppressor (especially to polynucleotide sequence encoding a transcription suppressor (especially trevention and treatment of viral cancers and lentivirus (especially infection. Cancers which may be treated include those caused by members of the ras oncogene family and cancers associated with human papilloma virus (HPV), bovine papilloma virus (BPV) and HTLV-1 (human T cell lymphotropic virus-1). The present sequence is the protein encoded by the HW-6 ts gene; it can be used directly to treat the same diseases.

(Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                    Gene therapy for treatment of viral cancers or lentivirus infection - by transfection of cells with transcription suppressor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
                                                                                                        Transcription suppression; human cancer; ts gene; transformation; herpes helper virus; HHV-6; ras oncogene family; lentivirus; human appilloma virus; HPV; bovine papilloma virus; BPV; human T cell lymphotropic virus-1; HILV-1; HIV LTR promoter; infection; human immunodeficiency virus; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
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                                                                                     HHV-6 transcription suppressor protein.
                                                                                                                                                                                                                                                                                                                                      Rosenthal LJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat Protein S32426, SEQ ID NO 4016.
 AAW13494 standard; protein; 490 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADES8145 standard; protein; 298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 2A; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 LSHRGGKKNTVSFIGP 339
                                                                                                                                                                                                                                                                                     95US-0001010P
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Best Local Similarity 56.2%,
Best Local 9; Conservative
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                            (GEOU ) UNIV GEORGETOWN
                                                                                                                                                                                                                                                                                                                                     Araujo JC, Doniger J,
                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-118825/11.
                                                                                                                                                                                     Human herpesvirus 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 490 AA;
                                                                                                                                                                                                           409702841-A1
                                                                                                                                                                                                                                                             09-JUL-1996;
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                                                27-AUG-2003
21-OCT-1997
                                                                                                                                                                                                                                     30-JAN-1997
                         AAW13494;
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ADE58145
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence the expression of a polynucleotide sequence which is differentially expression of a polynucleotide or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polynpeptides or their antibodies. The polynucleotide or the compound that colypeptides or their antibodies. The polynucleotide or the compound to pain and a pharmaceutical composition comprising the one or more pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the sequence data for this patent did not form part of the printed expecification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page; 1017pp; English
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                                                                                 14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
14-AUG-2002; 2002WO-US025765
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Best Local Similarity 37.5%;
Matches 6; Conservative
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Human polypeptide SEQ ID NO 25456.

XX Human, cytokine; cell proliferation; cell differentiation; gene therapy; XW vaccine; peptide therapy; stem cell growth factor; haematopolesis; the transmission of the control of
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Query Match 41.6%; Score 47; DB 4; Length 99; Best Local Similarity 46.7%; Pred. No. 20; Autches 7; Conservative 2; Mismatches 6; Indels 0; Gaps

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2 CCVLNRQGGKRNAVL 16
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43 CCIINNSNGNRTIVL 57

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Search completed: May 28, 2004, 12:57:04 Job time: 48.5 secs

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381 ICCVLNRQGGKRNTVLFHGP 400
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chromosomal replic
succinoglycan bios
E1 protein - human
E1 protein - human
probable serine/th
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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                                         OM protein - protein search, using sw model
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1 ICCVLNRQGGKRNAVLFHGP 20
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	A/TILIC A/Refel A/Roces A/Resic A/Cross C/Super	A,TILLE: PATVOYINE GENOME: IN A,Reference number: A03695; M A,Accession: A03695 A,Molccule type: DNA A,Residues: 1.672 cRNO A,Cross-references: EMBL:X014: C,Superfamily: parvoyinus nonc	lrus gen ber: A03 8695 : DNA 72 <rho> 288: EMB</rho>	ome: nu 695; MU L:X0145 us nonc	ICLE IID:	A;Tille: Parvovirus genome: nucleolide sequence of H-1 and mapping A;Fille: Parvovirus genome: nucleolide sequence of H-1 and mapping A;Accession: A03695; MUID:83112183; PMID:6823009 A;Accession: A03695 A;Accession: DNA A;Molecule type: DNA A;Residues: 1-672 A;HO> A;Cross-references: EMBL:X01457; NID:g60993; PIDN:CAA25689.1; PID:cC. Superfamily: parvovirus noncapsid protein	ping or its genes by nybric PID:g60994; EMBL:J02198
ئچ فى	Query M. Best Lo	Match Local Sin	Similarity 95.99; Conservative	96.5% 95.0% vative	40 40	score 109; DB 1; Length Pred. No. 8.8e-10; ; Mismatches 1; Indel	672; .s 0; Gaps 0;
	à i	i i	1 ICCVLNRQGGKRNAVLFHGP	GKRNAVI	HH	P 20	

A; Molecule type: DNA

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Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative 0
                                                      88.5%;
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Best Local Similarity 90.0
Matches 18; Conservative
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A;Molecule type: DNA
A;Residues: 1-668 <REE>
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UYPVIM

noncaptaid protein NS1 - minute virus of mice (strain MVM1)

C;Species: minute virus of mice, murine parvovirus

R;Sahli, R.; McMaster, G.K.; Hirt, B.

R;Sahli, R.; McMaster, G.K.; Hirt, B.

Nucleic Acids Res. 13, 3617-3633, 1985

A;Title: DNA sequence comparison between two tissue-specific variants of the autonomous A;Restidues: 1-721 cSAH>

A;Residues: 1-721 cAST>

A;Accession: A29510; MUID:86115415; PMID:3502703

A;Accession: A29510; MUID:86115415; PMID:3502703

A;Accession: A29510

A;Molecule type: DNA

A;Residues: EMBL:M12032; NID:9332289; PIDN:AAA69566.1; PID:9825477

C;Superfamily: parvovirus noncapsid protein

C;Keywords: noncapsid protein
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C;Species: feline panleukopenia virus, FPLV
C;Species: feline panleukopenia virus, FPLV
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
R;Carlson, J; Rushlow, K.; Maxwell, I.; Maxwell, F.; Winston, S.; Hahn, W.
J, Virol. 55, 574-587, 1985
Jyitle: Cloning and sequence of DNA encoding structural proteins of the autonomous parv
A;Reference number: A03697; MuID:85265017; PMID:2991581
noncapeid protein NSI - minute virus of mice
C;Species: minute virus of mice, murine parvovirus
C;Date: 14-Nov-1983 #sequence_revision 28-Aug-1985 #text_change 08-Apr-1994
C;Dacession: A03696
R;Astell, C.R.; Thomson, M.; Merchlinsky, M.; Ward, D.C.
Nucleic Acids Res. 11, 999-1018, 1983
A;Title: The complete DNA sequence of minute virus of mice, an autonomous parvovirus.
A;Accession: A03696; MUD:83143341; PMID:6298737
A;Mocession: A03696
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95.0%; Pred. No. 9.4e-10;
tive 0; Mismatches 1; Indels
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A,Cross-references: EMBL:V01115
C,Superfamily: parvovirus noncapsid protein
C,Keywords: noncapsid protein
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nes 19; Conservative
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Best Local Similarity 95.0
Matches 19; Conservative
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noncapaid protein NS1 - mink enteritis virus (strain Abashiri)

Cispedies: mink enteritis virus, MEV
Cispedies: mink enteritis virus, MEV
Cispedies: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
Cistatesumari, T.; Horiuchi, M.; Hama, E.; Yaguchi, K.; Ishigurio, N.; Goto, H.; Shinage R;Kariatsumari, T.; 867-875, 1991
A;Title: Construction and nucleotide sequence analysis of an infectious DNA clone of the A;Reference number: A38350; MUID:91202123; PMID:2016597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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C;Species: feline panleukopenia virus, FPLV
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C;Accession: A36608
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: canine parvovirus (strain N)
C;Species: canine parvovirus, CPV
C;Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: A2962
R;Reed, A.P.; Jones, E.V.; Miller, T.J.
J. Virol. 62, 266-276, 1988
A;Title: Nucleotide sequence and genome organization of canine parvovirus.
A;Reference number: A29962; MUID:88062992; PMID:2824850
A;Residues: 1-392 <CAR>
A;Cross-references: EMBL:M10824; NID:g333474; PIDN:AAA47160.1; PID:g333475
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:M19296; NID:9333438; PIDN:AAA67459.1; PID:9333439 C;Superfamily: parvovirus noncapsid protein C;Keywords: noncapsid protein
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                                                                                                                                                 Length 392;
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Pred. No. 2.6e-08;
0; Mismatches 2; Indels
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90.0%; Pred. No. 2.6e-08;
tive 0; Mismatches 2;
                                                                                                                                              Score 100; DB 1;
Pred. No. 1.6e-08;
0; Mismatches 2;
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Query Match

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NAIternate names: left-ORF protein
C;Species: Aleutian mink disease virus
C;Accession: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 06-Jan-1995
C;Accession: A36760; A35529
R;Bloom, M.E.; Alexandersen, S.; Perryman; S.; Lechner, D.; Wolfinbarger, J.B.
J. Virol. 62, 2903-2915, 1988
A;Fitle: Nucleotide sequence and genomic organization of Aleutian mink disease parvovirus
A;Reference number: A36760; MUID:88275062; PMID:2839709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Gottschalck, E.; Alexandersen, S.; Storgaard, T.; Bloom, M.E.; Aasted, B. submitted to the EMBL Data Library, January 1994
A;Description: Sequence comparison of the non-structural genes of four different types of A;Reference number: S41434
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C;Date: 15-Sep-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C;Accession: S41861; S41436
                                            A,Accession: A48472
A,Status: preliminary
A,Molecule type: DNA
A,Robicule type: DNA
A,Robicules: 1-662 <BER>
A,Experimental source: strain NADL-2, ATCC VR-742
A,Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBIP:138790)
C,Superfamily: parvoxinus noncapsid protein
C,Keywords: noncapsid protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 86.7%; Score 98; DB 1; Length 662; Best Local Similarity 85.0%; Pred. No. 5.5e-08; Matches 17; Conservative 1; Mismatches 2; Indels
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        A; Reference number: A48472; MUID: 94025614; PMID: 8212598
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414 LCTILTKOGGKRGCIWFYGP 433
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A;Residues: 1-620 <BL2>
A;Cross-references: EMBL:M20036
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Best Local Similarity 50.0
Matches 10; Conservative
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Matches 10; Conservative
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A,Molecule type: DNA
A,Residues: 1-641 <GOT>
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R;Martyn, J.C.; Davidson, B.E.; Studdert, M.J.
J. Gen. Virol. 71, 2747-2753, 1990
A;Title: Nucleotide sequence of feline panleukopenia virus: comparison with canine parvo
A;Reference number: A36608; MUID:91073139; PMID:2174965
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A Mesidues: 1-660 cRAN-
B Mesidues: 1-670 cRAN-
B Mesidue
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Cispecies: porcine parvovirus
Cispecies: porcine parvovirus
Cipate: 31-Dec-1990 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
Cipate: 31-Dec-1990 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
Cipatesion: A36217, A48472; A33743
Rivasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W.
Airology 178, 611-616, 1990
A;Title: The complete nucleotide sequence of an infectious clone of porcine parvovirus, A;Reference number: A36217, MUID:91021005; PMID:2219713
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Virology 197, 86-98, 1993
A;Title: Genomic organization and mapping of transcription and translation products of
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C;Daces 30-Sep-1991 #text_change 16-Jun-2000
C;Dacession: A33302; B33402; A33743; A36217
R;Ranz, A.I.; Manclus, J.J.; Diaz-Aroca, E.; Casal, J.I.
J. Gen. Virol, 70, 2541-2553, 1989
A;Tille: Porcine parvovirus: DMA sequence and genome organization.
A;Reference number: A33302; MUID:90010964; PMID:2794971
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A;Experimental source: strain NADL-2
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A;Molecule type: DNA
A;Residues: 1-668 <MAR>
A;Cross-teerences: GB:X55115; NID:g60863; PIDN:CAA38910.1; PID:g60864
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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Pred. No. 2.6e-08;
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90.0%; Pred. No. 2...
0; Mismatches
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Matches 18; Conservative
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A; Accession: A33302

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A; Molecule type: DNA

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Gaps

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Length 726; 2; Indels

Score 55; DB 1; Pred. No. 0.69; 6; Mismatches

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Search completed: May 28, 2004, 13:00:58 Job time : 10.5 secs
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295 MLSKKTGKRNSTLFYGP 311
Query Match
Best Local Similarity 52.9%;
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                                                                                                          4 VLNRQGGKRNAVLFHGP
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A, Cross-references: EMBL:M14363; NID:g333454; PIDN:AAB59845.1; PID:g808803; EMBL:M21972; C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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Appearation is Sequence comparison of the non-structural genes of four different types A; Reference number: S41434
A; Reference number: S41434
A; Reference prealinary
A; Accession: S41439
A; Residue: prealinary
A; Residues: 1-641 < COT>
A; Cross-references: EMBL: Z29576
C; Genetics: S86/1
C; Superfamily: parvovirus noncapsid protein
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OUTPVS1

C;Species: bovine parvovirus

C;Species: bovine parvovirus

C;Species: bovine parvovirus

C;Species: bovine parvovirus

C;Species: Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999

C;Accession: C26.04

R;Chen, K.C., Shull, Bect., Moses, E.A.; Lederman, M.; Stout, E.R.; Bates, R.C.

A;Intle: Complete nucleotide sequence and genome organization of bovine parvovirus.

A;Reference number: A26104; MUID:87061184; PMID:3783814
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                              ene NS-1 protein - Aleutian mink disease virus
;Species Aleutian mink disease virus
;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Feb-1997
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C;Species: Aleutian mink disease virus
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Feb-1997
C;Accession: 841434
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Pred, No. 0.03;
4; Mismatches 6; Indels
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A;Introns: 586/1
C,Superfamily: parvovirus noncapsid protein
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P07303 murine minu
P07313 mameter par
P06431 feline panl
P274842 feline panl
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P274842 feline panl
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P12929 canine parv
P18547 porcine parv
P25502 porcine parv
P2649 human papil
O8wy91 homo agpien
P07296 human herpe
P9738 mus musculu
C00683 human herpe
P973887 caulobacter
C02049 human papil
P95078 mycobacteri
P07511 human papil
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GenCore version 5.1.6
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WNCS_PRVH

WNCS_PRVH

WNCS_MEVA

WNCS_PAVPK

WIH HPV25

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WITHES HUMAN

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NPD PYRAB
PCB2 MOUSE
PCB2 HUMAN
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Listing first 45 summaries
                                                 OM protein - protein search, using sw model
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1 ICCVLNRQGGKRNAVLFHGP 20
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Gapop 10.0 , Gapext 0.5
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1 VE1_HPV36 1 VE1_HPV17 1 HS70_ACHKL 1 HS70_CRELC 1 YDBH_ECOLI 1 EB30_CAEEL 1 MYH7_PIG 1 CH1A_ECOLI 1 NPD PYRFU 1 PYRK_AQUAE 1 RGR_MQUSE 1 CARA_BRUME	ALIGNMENTS	PRT; 668 eated) st sequence updat st amoutation upd	; Parvoviridae; Parvovirinae;	111 SEQUENCE FROM N.A. MEDILINE=91297126; PubMed=8517025; Diffoot N., Chen K.C., Bates R.C., Lederma M.; Diffoot N. chen K.C., Bates R.C., Lederma M.; I'the complete nucleotide sequence of parvovirus LuIII an localization of a unique sequence possibly responsible fencapsidation pattern."; Virology 192:339-345(1993).	vright. of Biol Institut tions as is not agreemen		5%; Score 109; 0%; Pred. No. 5. 0; Mismatche	TLFHGP 20         LFHGP 400	PRT; 672 eated) st sequence updat st annotation upd
36.3 609 36.3 609 36.3 652 36.3 673 36.3 1027 36.3 1935 35.4 251 35.4 251 35.4 251		STANDAF (Rel. 29, (Rel. 29, (Rel. 37, otein NS-1	uIII. NA viruses 5339;	DM N.A. 97126; PubMec Chen K.C., I Le nucleotid n of a unique n pattern." 2:339-345(19)	This SWISS-PROT entry is copbetween the Swiss Institute the Buropean Bioinformatics use by non-profit institumodified and this statement entities requires a license or send an email to license	122 1000 00	th 96. Similarity 95. 19; Conservative	ICCVLNRQGGKRNAVLFHGP 	TANDAR . 07, . 11,
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nes 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-- FUNCTION: Seems necessary for viral DNA replication.
-- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sahli R., McMaster G.K., Hirt B.;
"DNA sequence comparison between two tissue-specific variants of the autonomous parvovirus, minute virus of mice.";
Nucleic Acids Res. 13:3617-3631 (1985).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
"The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=86115415; PubMed=3502703;
Astell C.R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice, MVM(i), and comparison with the DNA sequence of the fibrotropic
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10794;
                                                                                                                 Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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0; Mismatches 1; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
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EMBL; M12032; AAA69567.1; -.
InterPro; IPRO01257; Pervo NS1.
Pfan; PF01057; Pervo NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
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I -> L (IN REF. 2).
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                                                                           Murine minute virus (strain MVMi) (Murine parvovirus)
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J. Virol. 57:656-669(1986)
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DE Noncapt

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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=10799;
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96.5%; Score 109; DB 1; Length 672;
Best Local Similarity 95.0%; Pred. No. 5.5e-10;
Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
1-JUL-19966 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
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                                                                                                                                                                                                                                                                                        EMBL, V01115; CAA24309.1; ALT_INIT.
PIR, A03696; UYPV1M.
TRANSPAC; T02375; -
Interpro; PR01057; Parvo_NS1.
Pfam; PP01057; Parvo_NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
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12F331142F72AA6D CRC64;
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95.0%; Pred. No. 5.5e-10;
tive 0; Mismatches 1;
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J. Gen. Virol. 72:867-875(1991).
--- FUNCTION: Seems necessary for viral DNA replication.
--- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                               Virology 183:195-205(1991).
-1- FUNCTION: Seems necessary for viral DNA replication.
-1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                      "Mapping specific functions in the capsid structure of canine
parvovirus and feline panleukopenia virus using infectious plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91202123; PubMed-2016597;
Kariatsumari T., Horiuchi M., Hama E., Yaguchi K., Ishigurio N.
Goto H., Shinagawa M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses, ssDNA viruses, Parvoviridae, Parvovirinae, Parvovirus, NCBI_TaxID=10793,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 100; DB 1; Length 668; Pred. No. 1.6e-08; 0; Mismatches 2; Indels
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1-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last amnotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
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443 I -> V (IN REF. 2).
575 I -> N (IN REF. 2).
76768 MW, 4F8FEA3EEG2D2AE7 CRC64;
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Gen. Virol. 71:2747-2753 (1990)
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                                                                                                                            MEDLINE=91272479; PubMed=1647068
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InterPro; IRR0013593; AAA ATPase.
InterPro; IPR001257; Parvo NSI.
Pfam; PF01057; Parvo_NSI; 1.
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90.0%;
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Best Local Similarity 90.0
Matches 18; Conservative
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575
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575
668 AA;
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                                                                                                                                                                                "Mapping specific
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P27438;
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MEDILINE-82556301; PubMed=2991581;
MEDILINE-8255617; PubMed=2991581;
Carlson J., Rushlow K., Maxwell I., Maxwell F., Winston S., Hahn W.;
"Cloning and sequence of DNA encoding structural proteins of the autonomous parvovitus feline panleukopenia virus.";
J. Virol. 55:574-587(198).
-i- FUNCTION: Seems necessary for viral DNA replication.
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NCBI_TaxID=10786;
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1-JAN-1988 (Rel. 06, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
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43971 MW; B875ADDB4977F616 CRC64;
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01-MAR-1992 (Rel. 21, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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MEDLINE=91073139; PubMed=2174965;
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InterPro; IPRO013593; AAA ATPase.
InterPro; IPRO01257; Parvo_NSI.
Pfam; PF01057; Parvo_NSI; I
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392 AA;
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ID _VNCS_FPV
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Gaps

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382 IACVLNROGGKRNTVLFHGP 401

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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Submitted (NG-1990) to the EMBL/GenBank/DDBJ databases.
-|- FUNCTION: Seems necessary for viral DNA replication.
-|- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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Reed A.P., Jones E.V., Miller T.J.;
"Nucleotide sequence and genome organization of canine parvovirus.";
J. Virol. 62:266-276(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 88.5%; Score 100; DB 1; Length 668; Best Local Similarity 90.0%; Pred. No. 1.6e-08; Matches 18; Conservative 0; Mismatches 2; Indels
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76764 MW; DE2CCEA69D2A63A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                     TP (POTENTIAL).
DBD5F9E92113685C CRC64;
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01-0CT-1989 (Rel. 12, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
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InterPro; IRR0013593; AAA_ATPase.
InterPro; IPR001257; Parvo_NSI.
Pfam; PF01057; Parvo_NSI; 1.
                                                                                                EMBL, D00765; BAA00662.1; -.
PIR, A38350; UYPVME.
InterPro; IPR0013593; AAA ATPase.
InterPro; IPR001257; Parvo NSI.
Pfam; PP01057; Parvo NSI; I.
SMART; SM00382; AAA; I.
                                                                                                                                                                                                                                                                                                                                                                                     76736 MW;
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Matches 18; Conservative
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AC 01-0CT

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                   STATEMENT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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G -> R (IN REF. 2).

K -> R (IN REF. 2).

C -> V (IN REF. 2).

TALTQHARFSNTDT -> NLHLTPTPPDSAIRTP (IN
                                                                                                                                                                                                                                                                                                   MEDLINE=91021005; PubMed=2219713;
Vanedevedenarya J., Basak S., Srinivas R.V., Compans R.W.;
"The complete nucleotide sequence of an infectious clone of porcine
parvovitus, strain NADL-2.";
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                                                                                                            Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=10797;
                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=90010964; PubMed=2794971;
Ranz A.I., Manclus J.J., Diaz-Aroca E., Casal J.I.;
Ranz Parvovirus: DNA sequence and genome organization.";
J. Gen. Virol. 70:2541-2553(1989).
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85.0%; Pred. No. 3.4e-08;
ive 1; Mismatches 2; Indels
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             P18547; P22965;
01-NOV-1990 (Rel. 16, Created)
10-NOV-1990 (Rel. 16, Last anguence update)
15-DEC-1998 (Rel. 37, Last anguetion update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
660 AA.
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295 MLSKKTGKRNSTLFYGP 311
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J. Virol. 60:1085-1097(1986)
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                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96183900; PubMed=8642680;
Bergeron J., Hebert B., Tijssen P.;
Identification of the Allotropic determinant and comparison with those of NADL-2 and field isolates.";
J. Virol. 70:2508-251851996).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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-i- FUNCTION: Seems necessary for viral DNA replication.

-i- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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Viruses, ssDNA viruses, Parvoviridae, Parvovirinae, Parvovirus.
NCBI_TaxID=10783;
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1-FPB-1996 (Rel. 31, Last sequence update)
15-DBC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
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75591 MW; B53F76D9F9FBD613 CRC64;
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MEDLINE-88275062; PubMed=2839709;
Bloom M.E., Alexandersen S., Perryman S., Lechner D.,
                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapel protein NS-1 (Nonstructural protein NS1).
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                             662 AA
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                                                                                                                                                                                                                                                 Porcine parvovirus (strain Kresse) (PPV)
                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=73487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
VNCS_ADVG
ID VNCS_ADVG
AC P24030;
                             PAVPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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use by non-profit institutions as long as its content is in no walfied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@18b.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine parvovirus (BPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete nucleotide sequence and genome organization of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.7%; Score 55; DB 1; Length 726; 52.9%; Pred. No. 0.38; 2; Indels tive 6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                           InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDILINE-87061184; PubMed=3783814;
MEDILINE-87061184; PubMed=3783814;
MEDILINE-87061184; PubMed=3783814;
Bates R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 60.2%; Score 68; DB 1; Length 590 Local Similarity 50.0%; Pred. No. 0.0023; les 10; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            439 ATP (POTENTIAL).
67364 MW; 9898818AFD5343B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 317 ATP (POTENTIAL).
726 AA; 81189 MW; 42659A611A3AP038 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1988 (Rel. 07, Created)
1-APR-1988 (Rel. 07, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncappid protein NS-1 (Nonstructural protein NS1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                726 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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us-10-069-056-13.rsp

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                                                                                      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Rlausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Mochan P.J., McKarnan K.J., Mallek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Nillalon D.K., Maran D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A., Schwitz, Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young M., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska W., Smailus D.E.,

M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

M. Maran A., Schein J.E., Jones S.J.M., Marra M.A.,

M. Maran A., Schein J.E., Jones S.J.M., Marra M.A.,

M. Maran A., Schein J.E., Jones S.J.M., Marra M.A.,

M. Maran A., Schein J.E., Jones S.J.M., Marra M.A.,

M. Maran A., Schein J.E., Jones S.J.M., Marra M.A.,

M. Maran A., Schein J.E., Jones S.J.M., Marra M.A.,

M. Maran A., Schein J.E., Jones S.J.M., Marra M.A.,

M. Maran A., Schein J.E., Jones S.J.M., Marra M.A.,

M. Maran A., Schein J.E., Skalska U., Smailus D.E.,

M. Maran A., Schein J.E., Jones S.J.M., Marra M.A.,

M. Maran A., Schein J.E., Scheil M. I., Skalska U., Smailus D.E.,

M. Maran A., Schein J. Maran M. Marra M.A.,

M. Maran A., Scheil J. M. Maran M.A.,

M. Maran A., Scheil J. M. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 221-577 FROM N.A.

SEQUENCE OF 221-577 FROM N.A.

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sudo H.,

Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabo S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.;

Ninomiya K., Iwayanagi T.;

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECURNCE OF 221-577 FROM N.A.
MEDLINE=20272150; PubMed=10810093;
Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
Lai G.-Hictication of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49.5; DB 1; Length 577;
Pred. No. 2.3;
2; Mismatches 4; Indels •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40660A5ACDD0A7C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S -> G (IN REF. 1).
L -> P (IN REF. 3 AND 4).
R -> M (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THAP-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AP258556, AAC23759.1; -.
EMBL, BC000247, AAH00247.1; ALT INIT.
EMBL, BC0002439, AAH009439.1; ALT_INIT.
EMBL, AX001216; BAA91560.1; ALT_INIT.
EMBL, AR32970; AAD27745.1; -.
                                                  TISSUE=Brain, and Eye;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62889 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ); IPRO06612; DUF_DM3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.8%;
                      58-577 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:23187; THAP4.
InterPro; IPR006612; DUF_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zinc-finger; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
59
121
261
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SMART; SM00692; DM3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261
413
577 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90281611; PubMed=2162112;
Kiyono T., Adachi A., Ishibashi M.;
Virola J., Infered from its DNA sequence.";
Viroloy 177401-4055(1990).
-1- FUNCTION: ATP-DEDENDENT DNA HELICASE REQUIRED FOR INITIATION OF VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
PROTEIN THE BI-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH CONTAINS BINDING SITES FOR BOTH PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfan, PF00519; E1; 1.
Pfam; PF00524; E1 N; 1.
Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qin W.X., Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Wan D.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gu J.R.; "Novel human cDNA clones with function of inhibiting cancer cell growth."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.2%; Score 50; DB 1; Length 605; 80.0%; Pred. No. 2; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (POTENTIAL).
70010193AE041730 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THA4 HUMAN STANDARD; PRT; 577 AA. Q8WY91; Q9NW26; Q9Y325; 10-OCT-2003 (Rel. 42, created) 11-OCT-2003 (Rel. 42, Last sequence update) 11-OCT-2004 (Rel. 43, Last annotation update) THAP domain protein 4 (PP238) (CGI-36).
                                                                                                               (Rel. 19, Created)
(Rel. 19, Last sequence update)
(Rel. 36, Last annotation update)
                                                             605 AA.
                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M32305; AAA46978.1; -.
PIR; C35324; W1WL47.
InterPro; IPR001177; Papillom_E1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      605 AA; 69185 MW;
                                                                                                                                                                                                                                            Human papillomavirus type 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   425 KRNCILFHGP 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440
                                                                                                                                                                                                  Replication protein El.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 KRNAVLFHGP 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            Papillomavirus.
NCBI_TaxID=10594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                       01-AUG-1991
                                                                                                                                              01-AUG-1991
15-JUL-1998
                                                             VE1 HPV47
P22419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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RESULT 14 THA4 HUMAN

셤 à

Matches

THAP4.

A RAP REPAREMENT OF THE REPARE

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Gaps

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us-10-069-056-13.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virology 209:29-51(1995).
-!- SIMILARITY: TO DNA REPLICATION PROTEIN (REP) OF ADENO-ASSOCIATED VIRUS 2 (AC P03132).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.,
"The DNA sequence of human herpesvirus-6: structure, coding content,
and genome evolution.";
                                                                                                                                                                                                                                                                                                                                              MEDLINE=91226542; PubMed=1851252;
Thomson B.J., Efetathiou S., Honess R.W.;
"Acquisition of the human adeno-associated virus type-2 rep gene by
human herpesvirus type-6.";
Nature 351:78-80(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92333248; PubMed=1321205;
Thomson B.J., Honess R.W.;
"The right end of the unique region of the genome of human herpesvirus 6 Ul102 contains a candidate immediate early gene enhancer and a homologue of the human cytomegalovirus US22 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB 1; Length 490;
Pred. No. 2.4;
3; Mismatches 4; Indels
                                                                                                                                                                                                         U94 OR REP OR HCLF2.

Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JQ1630; JQ1630.
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; 1.
SEQUENCE 490 AA: 55848 MW; 221CE58165187C1F CRC64;
                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein U94.
                                                                                                                      490 AA.
                   3 ICCAAVNCSNRQGKGEKRAVSFH 25
1 ICCVL----NROG-GKRNAVLFH 18
                                                                                                                      PRT;
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MEDLINE=95266321; Pubmed=7747482;
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J. Gen. Virol. 73:1649-1660(1992)
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Best Local Similarity 56.2
Matches 9; Conservative
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                                                                                                                      VU94 HSV6U
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VU94_HSV6U
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Search completed: May 28, 2004, 12:57:43 Job time : 7.75 secs

324 LSHRGGKKNTVSFIGP 339

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us-10-069-056-13.rspt

Title: Perfect score:

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Minimum DB Maximum DB

Database

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P89514 feline pani
071157 rat parvovi
096602 aleutian mi
065023 aleutian mi
065020 aleutian mi
085020 aleutian mi
08707 minute viru
092en5 arthrobacte
09199 ephdatia f
082e7 nitrosomona
01229 saccharomyc
08120 leptospira
067671 goose parvo
08128 muscovy duc
067671 goose parvo
08128 muscovy duc
06765 goose parvo
08761 goose parvo
08799 seisseria m
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08799 neisseria m
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09851 arabidopsis
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089290 ralstonia s
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Ball-Goodrich L.J., Johnson E., Jacoby R.;
Ball-Goodrich L.J., Johnson E., Jacoby R.;
"Divergent replication kinetics of two phenotypically different parvoviruses of rate;"
J. Gen. Virol. 82:537-546(2001).
EMBL; AF317513; AAK27438.1; -.
Interepro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=155025;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Nonstructural protein 1 (Fragment)
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Local Similarity 95.0 es 19, Conservative
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Copyright (c) 1993.- 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1 ICCVLNRQGGKRNAVLFHGP 20
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SECURNCE FROM N.A.
MEDLINE=94365951; PubMed=8083985;
Ball-Goodrich L.J., Johnson E.;
"Molecular characterization of a newly recognized mouse parvovirus.";
J. Virol. 68:6476-6486(1994).
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=12441;
[1]
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=35340;
                                     ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus
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                                                                                                                        Brown D.W., Like A.A.; "Sequence of a Diabetogenic Parvovirus of Rats."; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ball-Goodrich L.J.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases
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IIICETPO; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SEQUENCE 672 AA; 76112 MW; 31C6365276727363 CRC64;
                                                                                                                                                                               EMBL; U79033; AAB38326.1; -.
InterPro; IRR001257; Parvo NS1.
PFam; PF01057; Parvo NS1; I.
SEQUENCE 672 AA; 76056 MW; 0299B36871A0A10A CRC64;
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96.5%; Score 109; DB 12;
Best Local Similarity 95.0%; Pred. No. 7.1e-10;
Matches 19; Conservative 0; Mismatches 1;
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01-NOV-1996 (TrEMBLrel. 01,
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01-DEC-2001 (TrEMBLrel. 19,
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Matches 19; Conservative
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SEQUENCE FROM N.A.
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                                                      NCBI_TaxID=12441;
                  Kilham rat virus.
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                                                                                  Kilham rat virus.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=12441;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=172385;
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Ball-Goodrich L.J., Leland S.E., Johnson E.A., Paturzo F.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-22120170; PubMed-12124471;
Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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EMBL, AF332882; AAM3275-1; -.

Interpro; IPR001257; Parvo NSI.

Pfam; PF01057; Parvo NSI; I.

SEQUENCE 672 AA; 76059 MW; 63D8B9EBF99E07B3 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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96.5%; Score 109; DB 12;
Best Local Similarity 95.0%; Pred. No. 7e-10;
Matches 19; Conservative 0; Mismatches 1;
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InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
NON TER
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J. Virol. 72:3289-3299(1998).
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Q8JV18

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RESULT 3
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11D Q8JV18
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DT 01-O
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P88899

RESULT 4
P88899
ID P888
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DT 01-M
DT 01-D
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InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; \(\bar{1}\).
SEQUENCE 672 AA; \(\bar{7}\)6201 MW; \(C2F1A7)1F6EF449A6\) CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          parvovirus.";
Nucleic Acids Res. 11:999-1018(1983)
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prototype strain.";
J. Virol. 57:656-669(1986).
                                                                                                       Local Similarity 95.0 es 19; Conservative
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Q84363
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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NCBI_TaxID=172386;
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                                                                                                                                                                                                                              96.5%; Score 109; DB 12; Length 672; 95.0%; Pred. No. 7.1e-10; ive 0; Mismatches 1; Indels
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SEQUENCE FROM N.A.

BEDLINE-22120170; PubMed=12124471;
Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
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MEDLINE=22120170; PubMed=12124471;
Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
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Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
                                                                               parvoviruses.";
J. Gen. Virol. 83:2075-2083(2002).

BMBL; AF321230; AAM93272.1; -.
Interpo; IRR01257; Parvo NS1.
Pfam; PP01057; Parvo NS1; I.
SEQUENCE 672 AA; 75987 MW; 2284611C20CDB6E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parvoviruses.";
J. Gen. Virol. 83:2075-2083(2002).
BMBL; AR332884; AAM93279.1; -.
Interpro; IPR001257; Parvo NSI.
Pfam; PP01057; Parvo NSI; I.
SEQUENCE 672 AA; 75988 MW; 52DF6549349CF3FD CRC64;
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Last annotation update)
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Last annotation update)
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J. Gen. Virol. 83:2075-2083(2002).
EMBL; AF332883; AAM93277.1; -.
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Les 19; Conservative
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                                                                                                                                                                                                                                Query Match
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Q8JV14
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Q8JV16
ID Q8JV
AC Q8JV
DT 01-0
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DT 01-0
DE NONS
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MEDLINE=87061199; PubMed=3783817;
MEDLINE=87061199; PubMed=3783817;
MORGAN W.R., Ward D.C.;
"Three splicing patterns are used to excise the small intron common all minute virus of mice RNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MVM(p);
MEDLINE=86115415; PubMed=3502703;
Astell C.R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice,
"MNA sequence of the lymphotropic variant of minute virus of mice,
MVM(1), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MVM(p);
MEDLINE=83143341; PubMed=6298737;
Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
"The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine minute virus (Murine parvovirus).
Viruses; ssDNA virušes; Parvoviridae; Parvovirinae; Parvovirus.
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96.5%; Score 109; DB 12; Length 672; 95.0%; Pred. No. 7.1e-10; ive 0; Mismatches 1; Indels (
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EMBL; J02275; AAA67108 1; -.

InterPero; IPRO01257; Parvo. NS1.

Pfam; PPG177; Parvo. NS1; 1.

SEQUENCE 721 AA; 81896 MW; 18391758E42F0DCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                Q84365;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Nonstructural protein.
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Last sequence update)
Last annotation update)
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Gaps

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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Feline panleukopenia virus (FPV).
Viruses; seDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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                                                                                                                                                                                                                                                                                                                                                          Length 668;
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Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB000065; BAA19024.1; -.
EMBL; AB000065; BAA19024.1; -.
GO; GO:0019012; C:virion; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
RO; GO:000165; Parvo_NS1.
RICEPPO; IPR001257; Parvo_NS1.
R Pfam; Pf0.1057; Parvo_NS1.
R SMART; SM00382; AAA, ATPE
NONSETLURAL Protein.
NONSETLURAL PROTEIN.
SEQUENCE 668 AA; 76769 MW; 0ECAFEGERE2ABDE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 2.4e-08;
0; Mismatches 2;
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Feline panleukopenia virus (FPV)
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Matches 18; Conservative
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[1]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                 STRAIN=PLI-IV;
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                                                                                                                         STRAIN=lymphotropic variant;
MEDLINE=86115415; PubMed=3502703;
MEDLINE=86115415; PubMed=3502703;
MEDLINE=86116415; PubMed=861818.;
"DNA sequence of the lymphotropic variant of minute virus of mice, MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nonstructural protein 1.
Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10786;
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NCBI_TaxID=10786;
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                             Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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                                                                                                                                                                                                                                           prototype strain.";

J. Virol. 570:656-669(1986).

EMBL; M12033, AAA6566.1; -.

PIR; A23008; UYPVIM.

InterPro; IPRO1257; Parvo NS1.

Pram; PPO1057; Parvo NS1; 1.

SEQUENCE 721 AA; 9FD29C327C7F4BBF CRC64;
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01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 96.5%; Score 109; DB 12; Best Local Similarity 95.0%; Pred. No. 7.6e-10; Matches 19; Conservative 0; Mismatches 1;
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EMBL; AB000062; BAA19023.1; -
GO; GO:0000166; F:nucleotide binding; IEA.
InterPro; IPR0013593; AAA APPase.
InterPro; IPR001257; Parvo NS1.
Pfam, PR01057; Parvo NS1.
SMART; SM0382; AAA; I.
SEQUENCE 668 AA; 76755 MW; 37ABDFD3470
       minute virus (Murine parvovirus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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Feline panleukopenia virus (FPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03,
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Best Local Similarity
Matches 18; Conserva
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                                                                                                     SEQUENCE FROM N.A.
                                                 NCBI_TaxID=10794;
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01-MAY-1997
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P89515
ID P89511
AC 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DT Nonst
OS Felin
OC Virus
OX NCBL
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P89516
D1 D P8951,
D7 O1-MA
D7 O1-MA
D7 O1-MA
D7 O1-MA
D7 O1-MA
D8 Nonst
OC Virus
OC Virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI TaxID=10786;
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88.5%; Score 100; DB 12; Length 668;
Best Local Similarity. 90.0%; Pred. No. 2.4e-08;
Matches 18; Conservative 0; Mismatches 2; Indels (
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                                                       Exignification (1947) to the EMBL/GenBank/DDBJ databases.

REMBL; AB000065; BAA19028.1; --

REMBL; AB000065; BAA19026.1; --

GO; GO:0019012; C:virion; IEA.

R ThterPro; IPR001253; AAA_TPase.

R InterPro; IPR001253; Parvo_NS1.

R Ther Pro; IPR01253; Parvo_NS1.

R Pfam; PF01057; Parvo_NS1; I.

R NONBELTUCTURAL Drotein.

R SEQUENCE 668 AA; 76755 MW; 008CED50178833EF CRC64;
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, #AB000015;
EMBL, #AB000016;
EMBL, #AB000016;
EMBL, #AB000016;
EMBL, #AB00016;
EMBL, #AB00016;
EMBL, #AB0016;
InterPro; IPR00125;
Parvo NS1.
Fam: PF01057;
Parvo NS1.
Fam: PF01057;
BAM;
SMART; SM00382;
AAA, 1.
SEQUENCE 668 AA; 76743 MW; 84A210104D9D5788 CRC64;
                                                                   to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches 18; Conservative
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Horiuchi M.;
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P89513
AC P8951
AC P8951
DT 01-MA
DE NORSE
RA SEQUE
RA S
SKARBRARRARS
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Search completed: May 28, 2004, 13:00:04 Job time : 33 secs

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APPLICATION NUMBER: 60/055,948
FILING DATE: 1997-08-18
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Sequence 2, Appli
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Sequence 12444, A
Sequence 12444, A
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Sequence 28671, A
Sequence 5318, Ap
Sequence 23996, A
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Sequence 10, Appl
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76.483 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-222-869-10

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US-09-422-869-6

US-09-744-960-2

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US-09-422-869-2

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US-09-422-869-2

US-09-422-869-2

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US-09-252-991A-23996

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Sequence 1673, Ap Sequence 1673, Ap Sequence 1673, Ap Sequence 9, Appli Sequence 31370, A Sequence 1672, Ap Sequence 1672, Ap Sequence 1672, Ap Sequence 9, Appli Sequence 11, Appli	Seguence 11, Appl
US-09-702-705-1673 US-09-716-457-1673 US-09-71-1673 US-09-71-1673 US-08-333-977-9 US-08-225-9911-31370 US-09-225-9911-31370 US-09-716-457-1672 US-09-716-457-1672 US-09-718-457-1672 US-09-718-457-1672 US-09-718-457-1672 US-09-328-352-5338 US-09-328-352-5338 US-09-328-352-5338 US-09-328-352-5338 US-09-328-311-9 US-09-378-074-9 PCT-US-97-97370-9 US-09-79-8-611-11	US-08-487-811A-11
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## ALIGNMENTS

TITLE OF INVENTION: 123 Human Secreted Proteins
ITTLE OF INVENTION: 123 Human Secreted Proteins
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER FILING DATE: 1999-07-07
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08 APPLICATION NUMBER: 60/055,722 APPLICATION NUMBER: 60/055,723 FILING DATE: 1997-08-18 Sequence 243, Application US/09227357 Patent No. 6342581 GENERAL INFORMATION:

3 CVLNROGGKRNAVLFHGP 20

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Gaps
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APPLICANT: OTANI, KENICHI
APPLICANT: ARDIG ENAIG
TITLE OF INVENITON: METHODS OF TREATMENT OF TYPE 2 DIABETES
TITLE OF INVENITON: METHODS OF TREATMENT OF TYPE 2 DIABETES
TILE REFERENCE: ARCD: 307
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER PILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VOY: 2.0
SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 3; Length 444; Pred. No. 53; 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                       Sequence 10, Application US/09422869 Patent No. 6235481
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Patent No. 6235481
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Best Local Similarity 47.1%;
Matches 8; Conservative
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APPLICANT: COX, NANCY J.
APPLICANT: SREENAN, SEAMUS
APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
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SEQ ID NO 8
LENGTH: 513
TYPE: PRT
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APPLICANT: COX, NANCY J.
APPLICANT: SREENAN, SEAMUS
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Best Local Similarity
Matches 8; Conserv
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; ORGANISM: Human
US-09-422-869-10
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US-09-422-869-8
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Patent No. 6551795

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45.5; DB 4;
Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Xaa equals stop translation US-09-227-357-243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                           EARLIER APPLICATION UNDBER: 60/055,950
EARLIER PILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
                                           FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ICCVLNRQGGKR-NAVLFHGP 20
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 40.3%;
1 Similarity 52.4%;
11; Conservative
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Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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US-09-252-991A-17004
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APPLICANT: POLONSKY, KENNETH S.
APPLICANT: POLONSKY, KENNETH S.
APPLICANT: OCA, NAOHISA,
APPLICANT: COX, NAOHISA,
APPLICANT: COX, NAOHISA,
APPLICANT: COX, NAOHISA,
APPLICANT: SREENAN, SEAMUS
APPLICANT: APPLICANT: COTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAENE I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARCD:307
CURRENT: APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER PILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN OF TYPE
SEQ ID NOS: 30
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 544; 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: COX, NANCHISA
APPLICANT: COX, NANCHISA
APPLICANT: COX, NANCY J.
APPLICANT: STEENAN, SEAMUS
APPLICANT: OTANI, KENICHI
APPLICANT: OTANI, KENICHI
APPLICANT: BELL, GRAEME I.
IITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
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Pred. No. 83;
2; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 672
                      Application US/09422869
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Patent No. 6235481
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ilarity 47.1%;
Conservative
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Best Local Similarity 47.1%;
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserva
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TITLE OF INVENTION: 18036, A No. 6620592el Calpain-Like Protease; TITLE OF INVENTION: and Uses Thereof; FILE REFERENCE: 35800/209290; CURRENT APPLICATION NUMBER: US/09/794,960; CURRENT APPLICATION NUMBER: US/09/794,960; CURRENT APPLICATION NUMBER: US/09/794,960; CURRENT FILING DATE: 2001-02-26; PRIOR APPLICATION NUMBER: US/09/185,333; PRIOR PILING DATE: 2000-02-28; NUMBER OF SEQ ID NOS: 6; SOFTWARE: FastSRQ for Windows Version 4.0; SEQ ID NO 2; LENGTH: 517
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                                                                                                                                                                                                                               APPLICANT: HORIKAWA, YUKIO
APPLICANT: ODA, NAOHISA
APPLICANT: ODA, NAOHISA
APPLICANT: ODA, NAOHISA
APPLICANT: CAN, NACY J.
APPLICANT: ZHOU, YUN-PING
APPLICANT: THORI SERMAN, SEAMUS
APPLICANT: HORIA, KENICHI
APPLICANT: HAIS, CRABE I.
APPLICANT: BELL, GRABE I.
APPLICANT: BELL, GRABE I.
APPLICANT: BELL, GRABE I.
CURENT HILL GRABE I.
CURENT APPLICATION NUMBER: US/09/422,869
CURENT FILING DATE: 1999-10-21
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEG ID NO 6
TANGTH: 517
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Pred. No. 63;
2; Mismatches 7; Indels
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                                                                                                                                                    Sequence 6, Application US/09422869
                         222 CCVLSPRAGARELGEFH 238
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222 CCVLSPRAGARELGEFH 238
2 CCVLNRQGGKRNAVLFH 18
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Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-794-960-2
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US-09-422-869-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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US-09-794-960-2
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JACOBAL 122-991A-28671

1 Sequence 28671, Application US/09252991A

2 Sequence 28671, Application US/09252991A

2 Sequence 28671, Application US/09252991A

3 RELATION 0. 6551795

3 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

3 TITLE OF INVENTION: AERUGANOSA FOR DIAGNOSTICS AND THERAPEUTICS

4 TITLE OF INVENTION: ABRUGANOSA FOR DIAGNOSTICS AND THERAPEUTICS

5 TITLE REFERENCE: 107196.136

5 CURRENT APPLICATION NUMBER: US 60/074,788

5 PRIOR PELING DATE: 1998-02-18

6 PRIOR PELING DATE: 1998-02-18

7 PRIOR PELING DATE: 1998-07-27

8 NUMBER OF SEQ ID NOS: 33142

8 SEQ ID NO 28671

9 LENGTH: 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 2; Length 232;
Pred. No. 39;
                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISOPPY disk
COMPUTER: ISOPPY disk
COMPUTER: IBM FC COMPACTIOLE
COMPUTER: IBM FC COMPACTIOLE
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,345
FILING DATE: 22-MAY-1995
CICLASSIFTCATION: 345
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A.
REGISTRATION NUMBER: 30742
REGISTRATION NUMBER: 30742
REGISTRATION NUMBER: 30764
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa US-09-252-991A-28671
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156 VCHVRNKRAGKEEPVVVH 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
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Best Local Similarity 38.9%;
Matches 7; Conservative '
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Best Local Similarity 57.1%;
Matches 8; Conservative
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            RY: U.S.A.
10036-2711
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Sequence 8212. Application US/09489039A

Sequence 8212. Application US/09489039A

Patent No. 66108B

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 656
                         Sequence 1244, Application US/09489039A
Sequence 12444, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PAPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12444
LENGTH: 710
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Patent No. 5831009
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Ullrich, Axel
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Axin B.
ITLE OF INVENTION: PHOSPHATASES PTP-D1
ITLE OF INVENTION: PHOSPHATASES PTP-D1
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 38.1%; Score 43; DB 4; Best Local Similarity 52.9%; Pred. No. 88; Matches 9; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.6%; Score 42.5; 62.5%; Pred. No. 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8212
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
, ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 CSSLSRSGGRRSA--FH 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CCVLNROGGKRNAVLFH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VLNRQGGKRNAV-LFH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :||| ||| || 4
46 ILNRVGGKENIVSLVH 61
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Best Local Similarity
Matches 10; Conserv
RESULT 9
US-09-489-039A-12444
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US-09-489-039A-8212
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US-08-446-345-38
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                                                                                                                                                                                                                        Score 42; DB 4; Length 572;
Pred. No. 1e+02;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rushlow, Keith E.
APPLICANT: Rushlow, Keith E.
APPLICANT: Rushlow, Keith E.
APPLICANT: Frank, Glern R.
APPLICANT: Frank, Glern R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Parrick J.
APPLICANT: Glines, Parrick J.
APPLICANT: Glines, Parrick J.
APPLICANT: Glines, MULEA PROTEINS, NUCLEIC ACID TITLE OF INVENTION: MULECULES AND USES THEREOF OWNERS OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
36.3%; Score 41; DB 3; Length 84;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
APLIGNE DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 23996 LENGTH: 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/906,769
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 99, Application US/08906769
Patent No. 6077687
GENERAL INFORMATION:
                                                                                                                         ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23996
                                                                                                                                                                                                                                                                                                                                                                           242 VLRROAGGRRADLRHHP 258
                                                                                                                                                                                                                                                                                                                             4 VLNROGGKRNAVLFHGP 20
                                                                                                                                                                                                                        Query Match 37.2%;
Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (303) 863-0233
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CCVLNRQGGKRNAV 15
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-906-769-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                    APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERABEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                              NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: misc_feature
) LOCATION: (B) LOCATION 1...384
); SEQUENCE DESCRIPTION: SEQ ID NO: 5318:
US-09-107-532A-5318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-252-991A-23996
; Sequence 23996, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: «Unknown»
                                                 Sequence 5318, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (781)893-5007
TELERAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5318:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 NGGĞĞARDGVTFHĞ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 NRQGGKRNAVLFHG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity ?
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                            US-09-107-532A-5318
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4 CCPTSRERGNRNRV 17

Search completed: May 28, 2004, 13:02:04 Job time: 14.5 secs

Sequence 29, A Sequence 29, A Sequence 25, A Sequence 29, A Sequence 29, A Sequence 25, Ap Sequence 27, Ap

Sequence 31,

Sequence 29, Appl Sequence 27, Appl Sequence 243, Appl Sequence 240, Appl Sequence 240, Appl Sequence 240, Appl Sequence 280, Appl Sequence 290, Appl Sequence 290, Appl Sequence 290, Appl Sequence 290, Appl

Perfect score:

ü

Run

Sequence:

Scoring table:

Database

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Sequence 200078, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REPERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-64-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 200078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_22697C.1.pep
US-10-424-599-200078
        12;
                                                                                                                                                                                                                                                                                                                                                                                                   US-09-953-351-39
US-10-080-376-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

44.2%; Score 50; DB:
Best Local Similarity 50.0%; Pred. No. 3.2;
Matches 8; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-317-832-130
Sequence 130, Application US/10317832
Publication No. US20030186337A1
GENERAL INFORMATION:
APPLICANT: Jean-Philippe Girard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : |::| ||| |:| |
24 IFNORGNKRNTVIFDG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VLNRQGGKRNAVLFHG
ORGANISM: Glycine max
                          -10-424-599-200078
                                                                                                                                                                                                                                                                       45.5
 Sequence 130, App
Sequence 25, Appl
Sequence 102, App
Sequence 6, Appli
Sequence 122, App
Sequence 9422, Ap
Sequence 9422, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 37, Appl
Sequence 31, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 200078,
                                                                                                              (without alignments)
160.719 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
                                                                                                 May 28, 2004, 12:57:09 ; Search time 34.75 Seconds
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-424-599-200078
US-10-317-832-130
US-10-317-832-130
US-10-317-832-102
US-10-317-832-102
US-10-188-186-122
US-10-138-977-9422
US-10-335-977-9423
US-10-335-977-9423
US-10-335-977-9423
US-10-335-977-9423
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US-10-080-376-31
US-10-082-671-37
US-10-097-100-31
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                       1151071 seqs, 279249464 residues
                                                                                                                                                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                   1 ICCVLNRQGGKRNAVLFHGP 20
                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 10
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Match Length DB
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THAP1 AND PAR4 PATHWAYS IN APOPTOSIS CONTROL

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JS-10-188-186-120
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Sequence 25, Application US/10317832

Sequence 25, Application US/10317832

Sequence 25, Application US/10317832

Sequence 25, Application US/10317832

APPLICANT: Jean-Philippe Girard

APPLICANT: Myriam Roussigne

APPLICANT: Sophia Kossida

APPLICANT: Francis Amalric

APPLICANT: Thomas Clouaire

TITLE OF INVENTION: NOVEL DEATH ASSOCIATED PROTEINS, AND

TITLE OF INVENTION: THAPI AND PAR4 PATHWAYS IN APOPTOSIS CONTROL

TITLE OF INVENTION: THAPI AND SAC ENTROL

TITLE OF INVENTION: THAPI AND PAR4 PATHWAYS IN APOPTOSIS

CURRENT APPLICATION NUMBER: 2002-12-10

PRIOR APPLICATION NUMBER: 2001-12-18

PRIOR FILING DATE: 2001-12-18
                                                 APPLICANT: Francois Amalric
APPLICANT: Thomas Clouaire
TITLE OF INVENTION: NOVEL DEATH ASSOCIATED PROTEINS, AND
TITLE OF INVENTION: THAPL AND PAR4 PATHWAYS IN APOPTOSIS CONTROL
FILE REFERENCE: BIOBANK.009A
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43.8%; Score 49.5; DB 14; Length 95;
Best Local Similarity 52.2%; Pred. No. 4.3;
Matches 12; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
43.8%; Score 49.5; DB 14; Length 90;
Best Local Similarity 52.2%; Pred. No. 4.1;
Matches 12; Conservative 2; Mismatches 4; Indels
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Publication No. US20030186337A1
GENERAL INFORMATION:
APPLICANT: Jean-Philippe Girard
APPLICANT: Sophia Kossigne
APPLICANT: Sophia Kossida
APPLICANT: Francois Amalric
APPLICANT: Transcois Amalric
APPLICANT: Transcois Lousire
TITLE OF INVENTION: NOVEL DEATH ASSOCIATED PROTEINS, AND
                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/317,832
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/341,997
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 263
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 263
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 95
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Myriam Roussigne
Sophia Kossida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
US-10-317-832-25
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-317-832-130
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                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 130
LENGTH: 90
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/10317832
; Sequence 6, Application US/10317832
; Publication No. US20030186337A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: Jean-Philippe Girard
    APPLICANT: Sophia Kossida
    APPLICANT: Sophia Kossida
    APPLICANT: Thomas Clousire
    APPLICANT: Thomas Clous
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-397.
CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/303046
PRIOR APPLICATION NUMBER: 60/303046
PRIOR PILING DATE: 2001-07-05
PRIOR FILING DATE: 2002-07-05
PRIOR FILING DATE: 2003-01
PRIOR FILING DATE: 2001-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49.5; DE
Pred. No. 9.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
; TITLE OF INVENTION: THAP1 AND PAR4 PATHWAYS; FILE REFERENCE: BIOBANK.009A; CURRENT APPLICATION NUMBER: US/10/317,832; CURRENT FILING DATE: 2002-12-10; PRIOR PILING DATE: 2001-12-18; NUMBER OF SEQ ID NOS: 263; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 102; LENGTH: 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
43.8%; Score 49.5;
Best Local Similarity 52.2%; Pred. No. 28
Matches 12; Conservative 2; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ICCVL----NROG-GKRNAVLFH 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 52.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-317-832-102
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US-10-317-832-6
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Gaps

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Indels

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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
PILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: US/10/335,977
PILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: MANER: MANDER: ANY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...280
SEQUENCE DESCRIPTION: SEQ ID NO: 9422:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVUE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)727-7400
TELEFOX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9422:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acids
            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                       16
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 CVLNRQGTRHNNYL 70
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                                                                                                         143 CCIINNSNGNRTIVL
                                                                    2 CCVLNRQGGKRNAVL
         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                              US-10-335-977-9422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-335-977-9423
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            Matches
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Publication No. US20040029789A1
| GENERAL INFORMATION:
| APPLICAMY: Anderson et al.
| TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
| TILE REPERENCE: 21402-397C
| CURRENT APPLICATION NUMBER: US/10/188,186
| CURRENT FILING DATE: 2002-07-02
| PRIOR PELIOR PATE: 2001-07-05
| PRIOR PELIOR PATE: 2001-07-05
| PRIOR APPLICATION NUMBER: 60/303046
| PRIOR APPLICATION NUMBER: 60/303046
| PRIOR APPLICATION NUMBER: 60/30308
| PRIOR APPLICATION NUMBER: 60/30308
| PRIOR PELING DATE: 2001-09-07
| PRIOR APPLICATION NUMBER: 60/30416
| PRIOR APPLICATION NUMBER: 60/304016
| PRIOR PELING DATE: 2001-07-09
| PRIOR PELING DATE: 2001-07-09
| PRIOR PELING DATE: 2001-07-13
| PRIOR PELING DATE: 2001-07-14
| PRIOR PELING DATE: 2001-07-04
| PRIOR PELING DATE
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PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/361133
PRIOR PLILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2001-07-09
PRIOR PLICATION NUMBER: 60/304502
PRIOR PLILNG DATE: 2001-07-11
PRIOR PLILNG DATE: 2001-07-11
PRIOR PLILNG DATE: 2001-07-13
PRIOR PLILNG DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/30861
PRIOR APPLICATION NUMBER: 60/308673
PRIOR PLILNG DATE: 2002-04-19
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-07-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-186-120
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ORGANISM: Homo sapiens
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Best Local Similarity
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SEQ ID NO 122
LENGTH: 343
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US-10-188-186-122
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LENGTH: 298
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0
LITE AND ACTUAL APPLICATION US/10335977
Sequence 9422, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9423, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 40.7%; Score 46; DB 12; Length 280; Best Local Similarity 64.3%; Pred. No. 47; Matches 9; Conservative 1; Mismatches 4; Indels
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Gaps
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Pred. No. 52;
1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 9;
Pred. No. 78;
5; Mismatches
SOFTWARE: UNIX

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: MANGES MANGE.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 9424:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
in NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...309
;
SEQUENCE DESCRIPTION: SEQ ID NO: 9424:
US-10-335-977-9424
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/09792630 Patent No. US20020168640A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/09953351; Publication No. US20030036643A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 LCGWVKREFNKRNAIWLYGP 171
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APPLICANT: Melander, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 40.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 CVLNROGTRHNNYL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-09-792-630-31
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION DIAGNOSTICS AND THERAPEUTICS
           RELATING TO HELICOBACTER PYLORI FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.7%; Score 46; DB 12; Length 299; 64.3%; Pred. No. 50;
                             DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...299

SEQUENCE DESCRIPTION: SEQ ID NO: 9423:

US-10-335-977-9423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                            COUNTRY: USA
ZETP: 0210-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: MANDE: MANDER: 36,207
REGISTRATION NUMBER: 37,207
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                              ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617)227-7400
TELEPAX: (617)42-4214
INFORMATION FOR SEQ ID NO: 9423:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 10031
                                               10031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                               STATE: Massachusetts
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                                                 NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                           CITY: Boston
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APPLICANT: Liu, Hong-Xiang
APPLICANT: Liu, Hong-Xiang
APPLICANT: Liu, Hong-Xiang
APPLICANT: Jin, Cheng He
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE CONSTRUCTION AND USE OF FUSION L)
FILE REFERENCE: A-70814/RFY/RMS/RMX
CURRENT APPLICATION NUMBER: US/10/097,100
CURRENT APPLICATION NUMBER: US/09/953,351
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 56
SOFTWARES PATENTIAN OF SEQ ID NOS: 56
SOFTWARES PATENTIAN OF SEQ ID NOS: 56
SOFTWARES PATENTIAN OF SEQ ID NOS: 56
LENGTH: 461
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Pred. No. 78;
5; Mismatches 7; Indels
                                                                                                DB 14; Length 461;
78;
                                                                                                                                              Indels
                                                                                              Score 46; DB 1
Pred. No. 78;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: May 28, 2004, 13:04:36
Job time : 35.75 secs
                                                                                                                                                                                                                                                                                                                                                   Sequence 31, Application US/10097100; Publication No. US20030068649A1; GENERAL INFORMATION; APPLICANT: Li, Min; APPLICANT: Melander, Christian
                                                                                                                                                                                                                       152 LCGWVKREFNKRNAIWLYGP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ICCVLNROGGKRNAVLFHGP 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 40.0%;
Matches 8; Conservative
                                                                                              Query Match
Best Local Similarity 40.0%;
Matches 8; Conservative
    ; TYPE: PRT
; ORGANISM: goose parvovirus
US-10-082-671-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: goose parvovirus US-10-097-100-31
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US-10-097-100-31
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APPLICANT: Liu, Hong-Xiang
APPLICANT: Liu, Hong-Xiang
APPLICANT: Jin, Cheng He
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE CONSTRUCTION AND USE OF FUSION
FILE REFERENCE: A-70814/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/953,351
PRIOR APPLICATION NUMBER: US 60/232,960
PRIOR FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn version 3.1
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Fublication No. US20030049647A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USE OF NUCLEIC ACID LIBRARIES TO CREATE TOXICOLOGICAL
TITLE OF INVENTION: USE OF NUCLEIC ACID LIBRARIES TO CREATE TOXICOLOGICAL
TITLE OF INVENTION: PROFILES
FILE REFERENCE: XEN/001
CURRENT APPLICATION NUMBER: US/10/082,671
CURRENT APPLICATION NUMBER: 60/270,781
PRIOR APPLICATION NUMBER: 60/270,781
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/10080376
Publication No. US20020172968A1
GENERAL INFORMATION:
APPLICANT: Li, Min
APPLICANT: Li, Min
APPLICANT: Dahiyat, Bassil I.
FILLE OF INVENTION: BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES
FILE REPERENCE: A-70295-2/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/080,376
CURRENT FILING DATE: 2000-02-19
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-02-22
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Best Local Similarity 40.0%; Pred. No. 78;
Matches 8; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 40.7%; Score 46; DB Best Local Similarity 40.0%; Pred. No. 78; Matches 8; Conservative 5; Mismatches
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SOFTWARE: Patentin version 3.1
SEQ ID NO 3.1
LENGTH: 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: goose parvovirus
US-10-080-376-31
                                                                                                                                                                                                                                                                                                          GRGANISM: goose parvovirus
US-09-953-351-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-10-080-376-31
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LENGTH: 461
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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2, 2004, 15:24:48 ; Search time 652 Seconds (without alignments) 3988.623 Million cell updates/sec OM nucleic - nucleic search, using sw model June Run on:

1 ggtcaagctattcgcattga.....aacagattgaaccaacacca 60 US-10-069-056-15 60 Perfect score: Sequence:

Scoring table:

3470272 segs, 21671516995 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

Total number of hits satisfying chosen parameters:

6940544

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database

em\_htg\_inv:\*
em\_htg\_other:\*
em\_htg\_mus:\* em\_vi:\* em\_htg\_hum:\* 9b ba: \*
9b ba: \*
9b ba: \*
9b px: \*
9b em\_ro:\* em\_sts:\* em\_pat:\* em\_un:\* em\_or:\* em\_p1:\* em om: \*: 0

Pred. No. is the number of results predicted by chance to have a

em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htgo\_other:\*

em\_htg\_rod:\* em\_htg\_mam:\* em\_htg\_vrt:\*

em\_htg\_pln:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Result No.	Score	Query Match	Length	DB	aı	ion
	-	09	100.0	9	و	AX137750	
	7	9	0	2019	ø	AX137751	ä
	3	8	٠	2019	9	AX137736	9
	4	58.4	7	2019	9	AX137739	σ
	ស	58.4	97.3	2019	9	AX137743	3 Sequenc
	ø	œ	۲.	2019	9	AX137747	747 Sequen
	7	œ		4773		HOU34255	5 Hamster
	Φ	58.4	7	5081	14	PAMVM2	15 Minute
	σ	œ	۲.	5149	14	Ö	75 Minut
	10	56.8	4.	4761	14	MVU34256	9
	11	è.	4.	5085	14	MVMICG	032 Minute
	12	9	₹.	5087	14	PAMVMI	31 Mouse
	13	'n	ä	4764	14	MOU34253	3 Mouse
	14	55.2	ď	4764	14	MOU34254	54 Mouse
	15	ī,	ä	5144	14	MPU12469	louse
	16	۳.	φ.	3530	14	AF317513	AF317513 Autonomou
	17	'n	σ.	3995	14	AF036711	
	18	ش	6	4795	14	AF332884	Rat
	19	ë.	6	4813	14	AF332882	AF332882 Rat minut
	20	۳.	6	4816	14	AF332883	AF332883 Rat minut
	21	ω,	6	4904	14	AF321230	AF321230 Kilham ra
	22	ω.	ė,	4927	14	KRU79033	U79033 Kilham rat
	. 23	ω.	6	5135	14	PVRSEQ	M81888 Parvovirus
	24	θ.	6	5176	14	PARH1	_
	25	9		4936	14	AF036710	T
	26	4.	4.	3524	9	104039	104039 Sequence 2
	27	44.6	4.	3524	9	108320	Sequence
	28	•	4	3670	14	POVCAP	7
	29	44.6	4.	4324	14	AY390557	57 Porcin
	30	•	4.	4948	14	5	Porcine
	31	44.6	4.	4973	14	POVG	
	32	44.6	4.	5034	14	POVNADL2	Porcine
	33	44.6	74.3	5075		POVTRANSPR	Porcine p
	34	42.4		2007	14	AB000048	8 Feline
	32	42.4		2007	14	AB000049	49 Feline
	36	42.4		2007	14	AB000051	51 Feline
	37	42.4	。	2007	14	AB000053	53 Feline
	38	42.4	ö	2007	14	AB000057	7 Feline
	39	42.4	。	2007	14	AB000058	58 Feline
	40	42.4		2007	14	AB000060	060 Feline
•	41	42.4	٥.	2007	14	AB000062	062 Feline
	42	42.4		0	14	AB000063	063 Feline
	43	42.4	٠.	8	14	90000	0065 Feline
	44	42.4		2007	14	0000	<b>000067 Felin</b>
	45	42.4	70.7	8	14	AB000069	AB000069 Feline pa

DNA AX137750 60 bp Sequence 15 from Patent EP1077260. AX137750 GI:14273923 RESULT 1
AX137750
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

PAT 30-MAY-2001

linear

ALIGNMENTS

1 Nucesch,J. and Rommelaere,J. Parvovirus ns1 variants Patent: EP 1077260-A 15 21-FEB-2001; Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts Mice minute virus Mice minute virus Viruses; BSDNA viruses; Parvoviridae; Parvovirinae; Parvovirus. REFERENCE AUTHORS TITLE JOURNAL

N

FEATURES

CDS

ORIGIN

RESULT 2 AX137751

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NTVLFHGPASTGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAĞNFGQ
QYNQFKAICSGQTIRIDQKGKGSKQIEPTPVIMTNENITYNRIGCERFPEHTQPIRD
RMLNIHITHTHEGDFGLVDKNBWPNICAWLVKNGYQSTWASYCAKWGKVPDWSENWAE
PKVPFPINLLGSARSPFTTPRSTPLSQNYALTPLASDLEDJALEPWSTPNTPVAGTAE
TQNTGEAGSKACQDGQLSPTWSEIEEDLRACKGAEPLKKDFSEPLNLD"
1381 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACCAACACCA 1440
                                                                                                               PAT 30-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSYKKELQEDELKSLQRGAETTWDQSEDMEWETTVDEMTKKQVF1FDSLVKKCLFEVL
NTKN1FPGDVNWFVQHEWGKDQGWHCHVL1GGKDFSQAQGKWWRRQLNVYWSRWLVTA
CNVQLTPAER1KLREIAEDNEWVTLLTYKHKQTKKDYTKCVLFGNMIAYYFLTKKKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSPPRDGGYPLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRI
QTKKEVSIKTTLKELVHKRVTSPEDWMMMQPDSYIEMMAQPGGENLLKNTLEICTLTL
ARTKTAPDLILEKAETSKLTNFSLPDTRTCRIFAFHGMNYVKVCHAICCVLNRQGGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT 30-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MAGNAYSDEVLGATNWLKEKSNQEVFSFVFKNENVQLNGKDIGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parvovirus ns1 variants
Patent: EP 1077260-A 4 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
                                                                                                                                                                                                                                                                                                                                                                                      Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts (DB)
                                                                                                                                                                                                                         Mice minute virus
Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mice minute virus
Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.3%; Score 58.4; DB 6; Length 2019; 98.3%; Pred. No. 6.2e-09; ive 0; Mismatches 1; Indels 0
                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Wildtype Parvovirus NS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAC39989.1"
/db_xref="GI:14273910"
/db_xref="REMTREMBL:CAC39989"
                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'organism="Mice minute virus"

    2019
/organism="Mice minute virus"

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/db_xref="taxon:10794"
                                                                                                                                                                                                                                                                                                                                             Parvovirus ns1 variants
Patent: EP 1077260-A 1 21-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4 from Patent BP1077260.
                                                                                                     AX137736 2019 bp
Seguence 1 from Patent EP1077260.
AX137736
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   Nueesch, J. and Rommelaere, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nueesch, J. and Rommelaere, J.
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AX137736
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CNVQLTPAERIKLKEIAEDNEWVTLLTYKHKQTKKDYTKCVLFGNMIAYYFLTKKKIS
TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRI
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PKVPTPINLLGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTFVAGTAE
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NSYKKELQEDELKSLQRGAETTWDQSEDMEWETTVDEWTKKQVFIFDSLVKKCLFEVL
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NTVLFHGPASTGKSIIAQAIAQAVGNVGCYNAANVNPPFNDCTNKNLIWVEEAGNFGQ
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Patent: BP 1077260-A 16 21-FEB-2001;
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Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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                                                                                       /mol_type="unassigned DNA"
/db_xref="taxon:10794"
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                                                                                                                                                       <1. .>60
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/db_xref="REWTREMBL:CAC39996"
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                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 60; DB 6; L
100.0%; Pred. No. 1.7e-09;
ive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 60; Conservative 0; Mismatches 0;
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Sequence 16 from Patent EP1077260.
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/db_xref="GI:14273926"
                       Location/Qualifiers
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TSPPROGGTELSSDSGHKTINFLKEGEBHLVSKLYTDDMRPETVETTVTTAQETKKKIS
QTKKEVAI KTTLKELVHKRVTSPEDHWMQPDSY I EMAQPGGENLLKNTLEI CTLTL
ARTKTPAEDL I LEKAETSKLTINESLPOTRTCR I PAFHGMYTKKCHAI CCVLINGGGKR
NTVLFHGPASTGKSI I AQAI AQAVGNVGCYNAANVNFPFNDCTNKNLI WVEBAGNFGQ
QVNQFKAI CSGQTIR I DOKGKGSKQI RETPVI MTTNENI TYNRI GCEBREHFHOPI RD
RMLI HLTHTLDGDFGLVDKNEWPHI CAMLVKNGYGTWASYCAKWGKVPDWSENWAE
PKVPPFI NILLGSARSPTTPKSTPLSQNYAL FPLASDLEDLALEPWSTPNTPVAGTAE
TQNTGEAGSKACQDGQLSPTWSEI EEDLRACFGARFLKKDFSEPLNLD"
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TYPPROGYTEASDSGHKTNFLKGEREHLJVSKLYTDDNRE PETVETTVTAPOETKGRI
OTKKRVS I KTTLKELVHKRVTS PEDWAMORODS Y I EMPAQPGGENLLKNTLE CTLTL
ARTKTAPDLI LIEKAETSKLTNFSLPDTRACR I PAFHGMNYVKVCHAI CCVLNRQGGKR
NYVLEHQBASTGKS I I AADA AQAVGNYGCYNANVIP PPROCTRINLI, WYVERGARGROONOFKRAL WYVERGARGROONOFKRAL WYVERGARGROONOFKRAL WYVERGARGROONOFKRAL STANDERARGROON OVNOFKAL CSCHOPLING AMANIA PRINCH I DOKGKGSKOL EPT MYTHRINI TVYR I GCERR PEHTQP I RD
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TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
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Patent: EP 1077260-A 8 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
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Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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                                                                                                'note="unnamed protein product"
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                                                  'note="Parvovirus NS1 variant"
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    . 2019
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/mol_type="unassigned DNA"
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Sequence 8 from Patent EP1077260.
AX137743
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CNVQLTPAERIKLREIAEDNEWVTLLTYKHKQTKKDYTKCVLFGNMIAYYFLTKKKIS
TSPPRDGGYFLSSDSGWKTNPLKEGERHLVSKLYTDDMRPETVETVTTAQETKRGRI
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NAVLFHGPASTGKSI I AQAI AQAGNVGCYNAANVNFPFNDCTNKNLI WVEEAGNFGQ
QYNQFKAI CSOQTI RI DQAGKGSKQI BETPVI MTTNBNI TYVRI GCEBR PEHTQPIRD
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PKVPPPI NILGSARS PFTTPKSTPLSQNYALTPLASDLEDLAIBDWSTPNTPVAGTAE
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NTKNIFPGDVNWFVQHEWGKDQGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRWLVTA
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                                                                                                                                                                                                                                                                                        PAT 30-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parvovirus ns1 variants
Patent: BP 1077260-A 12 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
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Mice minute virus
Viruses; 8sDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Viruses; seDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (bases 1 to 4773)
Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
                                                                                                           1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAAACAGATTGAACCAACACA
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Score 58.4; DB 6; Length 2019;
Pred. No. 6.2e-09;
0; Mismatches 1; Indels 0
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                                                                                                                                                                                                                                                                                        linear
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/note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Parvovirus NS1 variant"
                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 2019
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                                                                                                                                                                                                                                                                              Sequence 12 from Patent EP1077260.
AX137747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /proteIn_id="CAC39995.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nueesch, J. and Rommelaere, J.
                                                                                                                                                                                                                                                                                                                                                                  AX137747.1 GI:14273921
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          97.3%;
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Hamster parvovirus
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Best Local Similarity 98.3
Matches 59; Conservative
          Query Match
Best Local Similarity 98.3
Matches 59; Conservative
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Thu Jun

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HGTTOMGVNWVSEAIRTRPAQVGFCQPHNDFFASRAGFFAAFKVPADITOGVDKEANG
SVRYSYGKQHGENWASHGPAPERYTWDETSFGSGRDTKDGFTQSAPLVVPPPLMGILT
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YQVSAEDNGNSYMSVTKWLPTATGNMQSVPLITRPVARNTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="unnamed protein product; Protein sequence is in conflict with the conceptual translation; coding sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="nHLVLGWVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDEAYDQY
IKSGKNPYLYFSAADQRFIDQTKDAKDWGGKVGHYFFRTKRAFAPKLATDSEPGTSGV
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The complete DNA sequence of minute virus of mice, an autonomous
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1 (bases 1 to 5149)
                                                                                                                                                                                       2332. .2361
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                                                                                                                                                                                                                                                                                                                                   2354. .2398
/note="unnamed protein product; coding sequence"
                         :286. .2354
'note="unnamed protein product; coding sequence"
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Pred. No. 6.4e-09;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
                                                                                                                                              'db_xref="SWISS-PROT:P03137"
'translation="MAPPAKRAKRGKGLRDGWLVGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parvovirus
Nucleic Acids Res. 11 (4), 999-1018 (1983)
83143341
6298737
                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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Best Local Similarity 98.3%;
Matches 59; Conservative
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MVMPCG
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Minute virus of mice with two major open reading frames (genome).
V01115
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TTLKELVHKRVTSPEDWMMQPDSYIEMAQPGGENLLKNTLEICTLTLARTKTAFDL
ILEKAETSKLTNFSLPDTRTCRIFAFHGMNYVKVCHAICCVLNRQGGKRNTVLFHGPA
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TLPGDFGLVDKNEWPMI CAMLVKNGYQSTMASYCAKWGKVPDWSENWAEPKVPTPINL
LGSARSPFTTPKSTPLSQNYALIPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DELKSLORGAETTWDQSEDMEWETTVDEMTKKQVFIFDSLVKKCLFEVLNTKNIFPGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular characterization of newly recognized rodent parvoviruses J. Gen. Virol. 77 (Pt 5), 899-911 (1996) 96201434
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The complete DNA sequence of minute virus of mice, an autonomous
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1 (bases 1 to 5081)
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                                                                                                           Losses 1 to 4773)

Bassalsen, D.G.

Direct Submission
Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pathology, University of Missouri-Columbia, W213
Veterinary Medicine Building, Columbia, M0 65211, USA
Location/Qualifiers
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Pred. No. 6.4e-09;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                             /organism="Hamster parvovirus"
/mol type="genomic DNA"
/specific_host="Mesocricetus auratus"
/db_xref="taxon:42843"
          Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
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/mol_type="genomic DNA"
/db_ref="taxon:10794"
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Local Similarity 98.3%;
hes 59; Conservative C
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Mice minute virus
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RESULT PAMVM2

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SOURCE

ORIGIN

COMMENT

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/db_xref="G1:332294"

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KSENYCRIFNHYTTDTSVKGNMAKDDAHEQIMTPMSLVDANAGVWLQPSDWQYICNT

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NSMETLGFYPWARTIASPYRXYFCVDRDLSVTYTENQBGTVEHNVMGTFRGNMSQFFTI
                                                                                                                                                                                                                                                                                                                                                                            NSYKKELQEDELKSLQRGAETTWDQSEDMEWETTVDEMTKKQVFIFDSLYKKCLFEVL
NTRNIFPGDVNWFVQHEWGKDQGWHCHVLIGGKDFSQAQGKWWRRQLAVYWSRWLVTA
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ARTKTAFDLILEKAETSKLTNFSLPDTRTCRIFAFHGWNYWKVCHAICCVLNRQGGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OVNOFKAI CSGQTIR I DÖKGKGSKQI EPTPVIMTTNENI TVVRIGCEERPEHTOPI RD
RMLNIHLTHTLPGDFGLVDKNEWPMI CAWLVKNGYQSTWASYCAKWGKVPDWSENWAB
PKVPTPI NILIGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAE
TONTGEAGSKACQDGQLSPTWSEI BEDLRACFGAEPLKKDFSEPLNLD"
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DKEANGSVRYSYGKQHGENWASHGPAPERYTWDETSFGSGRDTKDGFIQSAPLVVPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTVL FHGPASTGKS I I AQA I AQAVGNVGCYNAANVNF PFNDCTNKNL I WVEEAGNFGQ
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                                                                                                                                                                                                                                                                                                                                                   translation="MAGNAYSDEVLGATNWLKEKSNQEVFSFVFKNENVQLNGKDIG#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTWNPVYQVSAEDNGNSYMSVTKWLPTATGNMQSVPLITRPVARNTY"
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gene="VP"
note="minor transcription start site"
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<2286. .2316
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                                                                                                                                                                                                                                                        'product="nonstructural protein"
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join(2286. 2316,2399. .4557)
/gene="VP1"
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|gene="VP1"
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/protein_id="AAA67110.1"
/db_xref="GI:825482"
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                                                                                                                                                                                                                                                                                  protein_id="AAA67109.1"
db_xref="G1:332295"
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/gene="VP"
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/gene="NS1"
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/gene="VP"
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'gene="VP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Original source text: Minute virus of mice (strain MVM(p)), passed in mouse 1 (variant A-9) cells.

The parvoviridae family cantains two groups that infect mammalian hosts: (i) defective (helper-dependent) adeno-associated viruses, and (ii) autonomous (helper-independent) parvoviruses. MVM is a member of the latter group. Both groups have been demonstrated to package both plus and minus strands (in separate particles) of the spands and minus strands (in separate of particles) of the in the latter group.

The sequence below corresponds to the plus (+) strand, also referred to as the C-strand. The minus (-) strand is also referred to as the V-strand.

The 3' and 5' termini both exhibit the potential for forming stable 'fold-back' hairpins; these sequences appear to play a role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replication [1].

The left and right halves of the genome encode two distinct, but overlapping transcriptional units. The transcripts can be summarized [1] (1 map unit (mu) = 51 bp):

R1 (4.8 kb): 4.5 mu - 46 mu; 46+ mu - 95 mu
R2 (3.3 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu
R3 (3.0 kb): 40 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu
R3 is the major transcript.

There are two major open reading frames, both on the plus (or C) strans. The left side ORF (261-2279) probably encodes a non-capsid protein of 85 kd; the right side ORF probably encodes the viral capsid proteins, VP1 (or A, 83 kd), VP2 (or B, 64 kd), and VP3 (or C, 61 kd). But because of uncertainties about the precise splice points in the transcripts, the exact starts, stops and (possible) intron boundaries are not known.

revision 4804 4870 a-65bp-a in [2]; as in [1] [2]
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FLSSDSGWKTNPLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRIQTKKEVSIK
TTLKELVHKRVTSPEDWMMQPDSYIEMMAQPGGENLLKNTLEICTLTLARTKTAFDL
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snqltmagnaysdevigatnwikeksnqevpspvpknenvqlingkdigwnsykkelqe
delkslqrgaettwoqsedmewettvdemtkkqvpipdslvkkclffevintknifpgd
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STGKS I I AQA I AQAVGNVGCYNAANVNPPFNDCTNKNL I WVEEAGNFGQQVNQFKA I C
SGQT I RI DQKGKGSKQ I EPTPV I MTTNENI TVVR I GCEER PEHTQP I RDRMLNI HLTH
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                                                                                                                                                                                                                                                                                     Morgan, W.R. and Ward, D.C.
Three splitting patterns are used to excise the small intron common
to all minute virus of mice RNAs
J. Virol. 60 (3), 1170-1174 (1986)
      2 (bases 1 to 5149)
Statil,C.R., Gardiner,E.M. and Tattersall,P.
DNA sequence of the lymphotropic variant of minute virus of mice,
MVM(i), and comparison with the DNA sequence of the fibrotropic
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/lab_host="mouse 1 (variant A-9) cell"
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/protein_id="AAA67108.1"
/db_xref="GI:825481"
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/strain="MVM(p)"
                                                                                                                                 prototype strain
J. Virol. 57 (2), 656-669 (1986)
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1. .5149
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/gene="NS1"
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/gene="NS1"
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1. .5085
/organism="Mice minute virus"
/mol_type="genomic DNA"
/isolate="lymphotropic variant"
/db xref="taxon:10794"
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/organism="Mice minute virus"
/mol type="genomic DNA"
/strain="Cutter"
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/product="nonstructural
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J. Virol. 570, 656-669 (1986)
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/gene="NS1"
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/gene="NS1"
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/gene="NS1"
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/translation="MSDGTSQPDSGNAVHSAARVERAADGPGGSGGGGGGGGUGVST
GSYDNQTHYRFLGDGWVEITALATRLVHLAMPKSENYCRIRVHNTTDTSVKGNWAKDD
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GGQAIKIYNNDLTACMMVAVDSNNILPYTPAANSMETLGFYPWKPTIASPYRYYFCVD
RDLSVTYENQEGTVEHNVMGTPKGMNSQFFTIENTQQITLLRTGDEFATGTYYFDTNS
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QVGFCQPHNDFEASRAGPFAAPKVPADITOGVDKEANGSVRYSYGKOHGENWASHGPA
PERYTWDETSFGSGRDTKDGFIQSAPLVVPPPLNGILTNANPIGTKNDIHFSNVFNSY
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I (bases 1 to 4761)
Besselsen,D.G., Pintel,D.J., Purdy,G.A., Besch-Williford,C.L.,
Franklin,C.L., Hook,R.R. Jr. and Riley,L.K.
Molecular characterization of newly recognized rodent parvoviruses
J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pathology, University of Missouri-Columbia, W213
Veterinary Medicine Building, Columbia, MO 65211, USA
1. .4761
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                                                                                                                                                                                                                                                /note="ORF2; putative"
/codon_start=1
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/db_xref="GI:825484"
/translation="MFNYLFYRPEITWF"
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/db_xref="G1:825483"
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                                                      'note="VP intron (alt.)"
                                                                                                                                                                                             translation="MVGWWGINV"
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                                                                                                         'note="ORF3; putative"
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/codon start=1
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/gene="VP1"
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/gene="VP"
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/gene="VP1"
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Besselsen, D.G.
                                  gene="VP"
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/ LTTAL 1 at 1 on = "MISGSESLDQGAKRWAMFKVYKQMLKSVTYPFFHSVSRDAQKE
SNQLTMAGNAYSDBYLGTTWMLKEKSNQBVFSFVFKTBDVQLAGKDIGWNYKKELQE
BLKSLQGABTTWDQSEDDMENESTVDBMTKKQVFTVDSLVKKCLFEVLSTRNTAPAD
VTWFVQHEWGCDGAHTCHVLIGGKDFSQAQGKWWRQLNVYWSRWLYTACNVQLTPAE
RIKLREIAEDSEWYTLLTYKHKQTKKDYTKCVLFGNMIAYYFLTKKKISTSPPRDGGY
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                                                                                                                                                                                                                                             MVMICG 5.005-JUL-1995 Sinute virus of mice (MVM(i)), a lymphotropic variant of MVM,
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TTLKELVHKRVTSPEDWMMQPDSYIEMMAQPGGENLLKVTLEICTLTLARTKTAFDL
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STGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAGNFGQQVNQFKAIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGOTIRIDŌKGKGSKOI EPTPVIMTNENITVVRIGCEERPEHTQPIRDRMLNIHLTH
TLPGDFGLVDKNEWPMICAMLVKNGYQSTWASYCAKWGKVPDWSENWAEPKVPTPINS
LGSARSPFTTPKSTPLSQNYAITPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses, sBDNA viruses, Parvoviridae, Parvovirinae, Parvovirus. (Dases 1 to 5085)
Astell, C.R., Gardiner, E.M. and Tattersall, P.
DNA sequence of the lymphotropic variant of minute virus of mice, MVM(1), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86115415
Original source text: Minute virus of mice (lymphotropic variant
MVM) DNA, clone pEG222.
Location/Qualifiers
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                                                                                                                             Length 4761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alternative splicing; capsid protein; complete genome; nonstructural protein.
Mice minute virus
Mice minute virus
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VERSION
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PAMVMI
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TITLE
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STKNIAPADVTWFVQHEWGKDQGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRWLVTA
                                                                                                                                        QTKKEVSIKTLKELVHKRVTSPEDWMMQPDSYIEMMAQPGGENLLKNTLEICTLTL
ATKTRAPELLILEKAETSKLTNSLEPDTRTKKT FREHGNATVKVCHALCCULRQGGGR
NTVLEHGPASTGKSI IA ADA IAQACGNGCYNAANVRPEPINGCTNKNL WVEBAGNFG
OVNQFKAICSGQTIRIDOKGKGSKQIEPTPVIMTTNENITVRIGCERPEHTQPIRD
RWLHHLTHLTBGDFROTENDRUMPWHTOKNYGYGFWAGYCKWGRKVPDWSENWAE
PRVPTPINGLGSARSFGFPDWRUMPWHTOKNYGYGFWAGYCKWGRKVPDWSENWAE
TQNTGEAGSKACQDGQLSPTWSEIEBDLRASDLAEDLALEPWSTPNTFVAGTAE
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LUGILITNAN PIGTKON DIHESVNFNS VOOSLTAR BENSPYVDGOG WOKELDLEHKRRLH
LITA PEVCKNAAPGQULVRLGENLTDOYDPNAATLSR LYTYGTFFWKKLTMRAKLRAN
TTWNPVYQVSVEDNGNSYMSVTKWLPTATGNMGSVPLITRPVARNTY"
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NSMETLGFYPWKPT IAS PYRYYFCVDRDLSVTYENQEGTIEHNVMGTFKGMNSQFFTI
                                                                                                     CNVQLTPAERIKLRIAEDSEWVTLLTYKHKQTKKDYTKCVLFGNMIAYYFLTKKKIS
TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRI
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TAQGSRHGATQMEVNWVSEAIRTRPAQVGFCQPHNDFEASRAGPPAAPKVPADVTQGV
                                                                                                                                                                                                                                                                                                                                                                note="major transcription start site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             transcription start
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join(2287. 2317,2400. 4558)
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db_xref="GI:825478"
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/gene="VP"
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/gene="VP1"
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/gene="VP"
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gene="VP"
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/gene="VP1"
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Viruses, seDNA viruses, Parvoviridae, Parvovirinae, Parvovirus.

1 (bases 1 to 5087)
Sahli,R., McMaster,G.K. and Hirt,B.
DNA sequence comparison between two tissue-specific variants of the autonomous parvovirus, minute virus of mice
Nucleic Acids Res. 13 (10), 3617-3633 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGQÂIKIYNNDLTACMAVAVDSNNILPYTPAANSMETLGFYPWKPTIASPYRYYFCVD
RDLSVTYENQEGTIEHNVMGTPKGMNSQFFTIENTQQITLLKTGDEFATGTYYFDTNP
VKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATQMEVNWVSEAIRTRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGILTNANPIGTKNDIHFSNVFNSY
GPLTAFSHPSPVYPQGQIMDKELDLEHKPRLHITAPFVCKNNAPGQMLVRLGPNLTDQ
YDPNGATLSRIVTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKWLP
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GSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCRIRVHTTDTSVKGNMAKDD
AHEQIWTPWSLVDANAWGVWLQPSDWQYICNTWSQLNLVSLDQSIFNVVLKTVTEQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVGFCQPHNDFEASRAGPFAAPKVPADVTQGVDREANGSVRYSYGKQHGENWAAHGPA
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Mouse parvovirus minute virus immunosuppressive variant genome ( =
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The genomes of MVMp and MVMi (immunosuppressive variant) have more than 96% of their sequence in common.

Data kindly reviewed (18-JUL-1986) by G. McMaster.

Location/Qualifiers
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Mice minute virus
Mice minute virus
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Pred. No. 2.2e-08; ·
0; Mismatches 2;
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/db_xref="taxon:10794"
1...116
/note="terminal hairpin region"
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                                                                                                                                                                                                                                                                              'translation="MFNYLFYRPEITWF"
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/db_xref="GI:825479"
                                                      translation="MVGWWGINV"
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                                                                                                                                    'note="ORF2; putative"
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                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                        2400. .>4558
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2795. .4558
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/gene="VP2"
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Best Local Similarity 96.7%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                 'number=2
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Query Match
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YLYFSAADQRFIDQTKDAKDWGGKVGHYFFRTKRAFARATDSEPGTSGVSRAGKRT
RPPAYIFINOQARAKKGLTSSAAQQSSQCTMSDCTSQPDGGNGVHSAARVERAADGPGGS
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GGGGSGGGGGVGVSTGSYDMOCHYRFLGDGWYBIAAARTLMHLMMPKGENYCRIRVHN
TTDTSVKGNMAKDDAHEQIWTPWSLVDANAWGWLQPSDWQYICNTWSQLALVSLDQE
IFWNYLKYTYDGOSGGGAIKTYNNDLTACWWANDSNNILEPTRAANSWETLGFFPWK
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DERATGTYYPDTNPVKLTHTWQTNRQLGQPPLLSTFPRADTDAGTLTAQGSRHGATQM
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GKQHGENWAAHGFAPERYTWDETASRRAGFFAARTPROTOGNEANGSWRYSY
GKQHLVRLGPRILTDQYDPNGATLSRIVTYGTFFWKGKLTMRAKLRANTTWNPVXQVSUE
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BREXTWDFSTRYBGSGRDTRDGFLQSAFLVVPPENGTLITAPRPTGTKONAPTGTKONTFNS
YGPLTAFSHPS PVVPGQTWDKELDLEHKPRLHITAPPVCKNNAPGQMLVRLGPNLTD
QYDPNGATLSRI VITYGTFFWKGKLTMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAHEQIWTPWSLVDANAWGVWLQPSDWQYICNTWSQLNLVSLDQEIFNVVLKTVTEQD
SGGQAIKIYNDLTACWMVAYDSNNILLPYTPAANSMETUGEYPWKPTIAA
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94.7%; Score 56.8; DB 14; Length 5087;
Best Local Similarity 96.7%; Pred. No. 2.2e-08;
Matches 58; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                         function="coat protein"
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                   note="TATA box"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2792. .4558
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/gene="VP2"
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/gene="VP1"
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    promoter
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LOCUS
DEFINITION
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KEYWORDS
SOURCE
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Mouse parvovirus 1c

Viruses, sabNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

Viruses, sabNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

Loases 1 to 4644)

Besselsen, D. G., Pintel, D. J., Purdy, G. A., Besch-Williford, C. L.,

Franklin, C. L., Hook, R. R. Jr., and Riley L. K.

Molecular characterization of newly recognized rodent parvoviruses

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1 (bases 1 to 4764)

Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L., Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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                                                                                                                                                                                                                                                   Direct Submission
Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pathology, University of Missouri-Columbia, W213
Veterinary Medicine Building, Columbia, MO 65211, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4764;
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1 Similarity 95.0%; Pred. No. 7.4e-08;
57; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 92.0%; Score 55.2; DB 14; 1 Similarity 95.0%; Pred. No. 7.4e-08; 57; Conservative 0; Mismatches 3;
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/mol type="genomic DNA"
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Besselsen, D.G.
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Best Local Similarity
Matches 57; Conserva
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/ FEARSTAIL DESCRIPTION OF SERVICE SEVENTED VOLNGKDIGW
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// Genne="VPPI"
// GENNES

                          mrul2469 Sharles 5144 bp DNA linear VRL 24-JAN-1995 Mouse parvovirus 1 complete genome, nonstructural protein 1 (NS1) gene, complete cds and capsid protein (VP1) gene, complete cds. 1179.49
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GTSGVSIAGKRTKPPAHIFINQARAKKKRASLAAQQRTQTMGAEGPDSGSAVQSAA
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DNQETLGFYPWTRPSPYRYYFNCDRSLSVTYTDQTGSIVDTMANASGLSSQPFTIE
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TROBRSGI TOJS ISSNBYTEATRVREAVOVGPCOPHDNFETSRAGP FKVYBVORANYOGN
EHDANGSLRYTYDGHGODWGSNNSKER FTWADA I SYGGRWADRC FINATPFTSPPAL
NNILTNSDP I GNYTALHYQNVPNSYGPLTAFPHPAP I Y POGQI WDKELDLEHK PRILHA
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TWNPVYQVSAQYQNENEYMSIHKWLPTATGNMQSIPLLSRPVARNTY"
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                                                                                                                                                                                                                                                                                      Mouse parvovirus 1

Windse parvovirus 1

Windses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

Mases 1 to 5144)

Mases 1 to 5144)

Mall-Goodfich, L. J. and Johnson, E.

Molecular characterization of a newly recognized mouse parvovirus

J. Virol. 68 (10), 6476-6486 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-JUL-1994) Lisa J. Ball-Goodrich, Section of Comparative Medicine, Yale University School of Medicine, New Haven, CT 06520-8016, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mouse parvovirus 1"
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265. .2283
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/Gome="NOTALE"
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/gene="VP1"
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Ball-Goodrich, L.J.
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92.0%; Score 55.2; DB 14; Length 5144; 95.0%; Pred. No. 7.4e-08;

Best Local Similarity

Query Match

ORIGIN

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Thu Jun 3 10:28:23 2004
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                                                                                                                  2, 2004, 15:24:48 ; Search time 145.25 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                            OM nucleic - nucleic search, using sw model
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	<pre>(without alignments) 1754.849 Million cell updates/sec</pre>	gec
Title: Perfect score:	US-10-069-056-15 60	
Sequence:	1 ggtcaagctattcgcattgaaacagattgaaccaacaca 60	

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IDENTITY NUC Gapop 10.0 , Gapext 1.0	3373863 seqs, 2124099041 residues	Total number of hits satisfying chosen parameters:
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Minimum Match Maximum Match Listing first	N. Geneseq. 29Jano4: 11. geneseqn1980s: * 2 geneseqn1990s: * 3: geneseqn2000s: * 4: geneseqn2001bs: 5: geneseqn2001bs: 6: geneseqn2002s: * 7: geneseqn2003bs: 9: geneseqn2003bs: 9: geneseqn2003bs: 9: geneseqn2003cs: 10: geneseqn2003cs: 10: geneseqn2004s: 10: ge
Post-processing: Minimum Match 0% Maximum Match 10 Listing first 45	Database : 1 2 2 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aad02804 Parvoviru	Aad02805 Parvoviru	Aad02801 Parvoviru	Aad02803 Parvoviru	Aad02797 Parvoviru	Aad02799 Parvoviru	Aan40252 Sequence	Aat15311 Non-atten	Aat15312 Attenuate	Aat88321 Attenuate	Aat88324 Attenuate	Aat88320 Canine pa	Aaf22299 BAC conta	Aaf22285 BAC conta	Aaf22282 BAC conta	Continuation (6 of	Abq68065 Listeria	Abq69966 Listeria	Continuation (12 o	Aav26084 Tomato pe	Abl15067 Drosophil	Abl15066 Drosophil	Aah05198 Human cDN
SUMMARIES	ΩI	AAD02804	AAD02805	AAD02801	AAD02803	AAD02797	AAD02799	AAN40252	AAT15311	AAT15312	AAT88321	AAT88324	AAT88320	AAF22299	AAF22285	AAF22282	AAF22303 5	ABQ68065_	ABQ69966	ABA03041 11	AAV26084	ABL15067	ABL15066	AAH05198
	DB	2	ស	ß	'n	S	Ŋ	н	7	7	7	~	~	m	m	m	m	9	ø	9	7	4	4	4
	Length	9	2019	2019	2019	2019	2019	3524	5049	5049	5049	5049	5049	85680	94618	95223	110000	2451	2451	110000	51952	1876	4365	747
de	Query Match	100.0	100.0	97.3	97.3	97.3	97.3	74.3	70.7	70.7	70.7	70.7	70.7	45.3	45.3	45.3	45.3	44.0	44.0	44.0	43.0	42.7	42.7	42.3
	Score	09	9	58.4	58.4	58.4	58.4	44.6	42.4	42.4	42.4	42.4	42.4	27.2	27.2	27.2	27.2	26.4	26.4	26.4	25.8	25.6	25.6	25.4
	Result No.	1	7	e	4	S	<b>9</b>	7	80	6	10	11	12	c 13	c 14	15	c 16	17	18	c 19	20	21	22	23

Abl18508 Drosophil	Adb07799 Alloiococ	Adb07801 Alloiococ	Aah15778 Human cDN	Aac76412 Human ORF	Abk94959 Human nov	Aad21290 Human pho	Continuation (5 of	Abx62995 Human act	Aah57512 Human kid	Aba12234 Human ner	Aax77013 Mouse Sel	Aax77012 Full leng	Aa846237 DNA encod	Ach33393 Human end	Aaz16901 Human gen	Aaf18259 Lung canc	Aas84526 DNA encod	Abl03944 Drosophil	Abl19270 Drosophil	Abl19268 Drosophil	Abl10478 Drosophil
ABL18508	ADB07799	ADB07801	AAH15778	AAC76412	ABK94959	AAD21290	ADB12064 04	ABX62995	AAH57512	ABA12234	AAX77013	AAX77012	AAS46237	ACH33393	AAZ16901 .	AAF18259	AAS84526	ABL03944	ABL19270	ABL19268	ABL10478
135 4	2385 8	2385 8	45 4	82 3	173 6	72 4	8 000	51 7	55 4	306 5	2 999	3667 2	12790 4	445 8	767 2	508 3	729 5	180 4	13521 4	505 4	146 4
67	23	23	25	40	22	101	_	ĕ	ĕ	306	_					25					290
42.3	42.0	42.0	42.0	42.0	42.0	42.0	42.0	41.7	41.7	41.0	41.0	41.0	41.0	40.7	40.7	40.7	.40.7	40.7	40.7	40.7	40.7
25.4	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25	25	24.6	24.6	24.6	24.6	24.4	24.4	24.4	24.4	24.4	24.4	24.4	24.4
24	52	56	27	58	59	30	31	32	33	34	35	36;	37	38	39	40	41	42	43	4,4	45
U								υ	υ	U				U	U	υ	U	υ	O	O	U

## ALIGNMENTS

AAD02804; 06-AUG-2003 31-MAY-2001 Parvovirus no NS1; non-stru	revised) (first entry)
2003 2001 rus no n-stru	revised) (first entry)
rus no n-stru	
n-stru 1 diae	Parvovirus non-structure protein 1 (NS1) variant (T463A) DNA fragment.
,	NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
Parvovirus. Synthetic.	
	<pre>Location/Qualifiers 160 /*tag= a /product= "Parvovirus NS1 variant (T463A) peptide" /note= "CDS does not include start and stop codon" /partial</pre>
mutation	replace(40, A) /*tag= b /note= "This location corresponds to position 1387 of the variant (T463A) DNA shown in AAD02805"
EP1077260-A1.	
21-FEB-2001.	
13-AUG-1999;	99EP-00115161, .
13-AUG-1999;	99EP-00115161.
(DEKR-) DEUT	KREBSFORSCHUNGSZENTRUM.
Nueesch J, R	Rommelaere J;
01-212 AAY72	WPI; 2001-212717/22. P-PSDB; AAY72709.
arvovi disea iption	Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
	EPI 07260-A1.  13-AUG-1999; 998  (DEKR-) DEUT KREBS  (Nueesch J, Rommel  WHI; 2001-212717//  P-SDB; AAY72709.  Novel parvovirus I  tumoral diseases, transcription acti

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therapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                                               The present sequence is a parvovirus non-structure protein 1 (NS1) variant (T463A) DNA fragment. The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytoctoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSI; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                  GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAACAACAACAACCA
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                                                                                                                                                                                                                                                                                             100.0%; Score 60; DB 5; Length 60; 100.0%; Pred. No. 1.5e-10;
                                                                                                                                                                                                                                                                                                                                       0; Indels
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/product= "NS1 variant (T463A) protein"
replace(1387, A)
/*tag= b
                                                                                                                                                                                  diseases. The variant DNAs are useful as vect (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                   Sequence 60 BP; 26 A; 13 C; 12 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                       Disclosure; Page 27; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 27-30; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD02805 standard; DNA; 2019
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                                                                                                                                                                                                                                                                                                                                            60; Conservative
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31-MAY-2001
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Synthetic.
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                                                                                                                                                                                                       therapy.
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AAD02805
ID AAD02805
ID AAD02805
ID AAD02805
ID AAD07
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XX NX NSI
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FT CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parvovirus non-structure protein 1 (NS1) variant (T363A) DNA
                                                 Length 2019;
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Sequence 2019 BP; 697 A; 389 C; 453 G; 480 T; 0 U; 0 Other;
                                                                                                    0; Indels
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replace(1187, A)
/*tag= b
                                              100.0%; Score 60; DB 5; ]
100.0%; Pred. No. 2.7e-10;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                            AAD02801 standard; DNA; 2019 BP
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                                                                                                       60; Conservative
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P-PSDB; AAY72706.
                                                 Query Match
Best Local Similarity
Matches 60; Conserv
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31-MAY-2001
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                                                                                                                                                                                                                                                                                             RESULT 3
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3

Parvovirus Synthetic

mutation

AAD02803;

RESULT

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1381 GGTCABACTATTGGCATTGATCABABGGBABAGGCAGCABCCAACAGATTGAACCAACAACAA 1440
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                                                                                                              NSI; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; ds.
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                                                                            Parvovirus non-structure protein 1 (NS1) wild-type DNA.
                                                                                                                                                                                                        Location/Qualifiers
1. .2019
/*tteg= a //tteg= a //product= "Parvovirus NS1 protein"
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                                       (first entry)
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Best Local Similarity 98.3<sup>3</sup>
Matches 59; Conservative
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                       (revised)
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P-PSDB; AAY72702.
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31-MAY-2001
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AAD02799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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tumoural disease; gene therapy; mutant; mutein; variant; ds.
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Pred. No. 9.2e-10;
                                                                                                                                                                                                                                                   Parvovirus non-structure protein 1 (NS1) variant (T394A) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2019 BP; 697 A; 389 C; 453 G; 480 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "NS1 variant (T394A) protein"
replace(1180, A)
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 22-24; 41pp; English
                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD02797 standard; DNA; 2019 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.3%;
                                                                                                                 AAD02803 standard; DNA; 2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-00115161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99EP-00115161
                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nueesch J, Rommelaere J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-212717/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY72708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1077260-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1999;
                                                                                                                                                                                          06-AUG-2003
                                                                                                                                                                                                            31-MAY-2001
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and

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Gaps

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Indels

9

therapy;

Synthetic

AAD02797

RESULT 5
AAD02797
ID AAD0
XX
AC AAD0

Query Match

Matches

g

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Location/Qualifiers

.2019

.ag= a /product= "NS1 v replace (847, A) /\*tag= b

mutation

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

Nueesch J, Rommelaere J;

WPI; 2001-212717/22 P-PSDB; AAY72704.

99EP-00115161 99EP-00115161

13-AUG-1999; 13-AUG-1999;

EP1077260-A1

21-FEB-2001

Claim 7; Page 11-14; 41pp; English.

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1 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAACAACAGACCAACACC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parvovirus; dog; vaccine; CPV; myocardial disease; enteric disease; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relative to control
disease in animals,
                                                                                                                                                                                                                                    Polypeptide obtd. by recombinant DNA methods - for vaccination against parvovirus infections in man and animals.
                                                                                                                                                                                                                                                                                                                      The inventors claim an immunologically active polypeptide for the development of vaccinal immunity against parvovirus infection. Also claimed are DNA sequences wholly or partly duplicative of defined sequences. The polypeptides are used in vaccines for conferring protection against parvovirus infections in man and animals. (Updated v24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This viral DNA is isolated from a non- attenuated CPV. The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

Pest Local Similarity 84.7%; Pred. No. 4e-05;

Matches 50; Conservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3524 BP; 1400 A; 719 C; 648 G; 757 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-attenuated canine parvovirus CPV-39 passage 5 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (s)
CPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Attenuated CPV strains contg. up to 4 mutation virus - useful as a veterinary vaccine against such as wild or domestic dogs.
                                                                                                                                                                                                                                                                                         Claim 10; Table II, Page 33-49; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parrish CR, Gruenberg A, Carmichael LE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 21-24; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
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                              84WO-US000063
                                                               83US-00459203.
                                                                                                                                                                                       WPI; 1984-201354/32.
P-PSDB; AAP40306, AAP40675.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canine parvovirus.
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                                                                                                                  (AMGE-) AMGEN
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                                19-JAN-1984;
                                                                 19-JAN-1983;
06-JAN-1984;
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02-AUG-1984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT15311;
                                                                                                                                                    Fox GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT15311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a DNA encoding parvovirus non-structure 1 protein (NS1) variant (S283A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAAACAGATTGAACCAAACACCA 60
                                                                                                                                                                                                                                                                                                                                                                                    Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence from the double-stranded replicative form DNA of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58.4; DB 5; Length 2019;
Pred. No. 9.2e-10;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2019 BP; 698 A; 389 C; 453 G; 479 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein envelope; immunogen; vaccine; antigen; epitope; ds
                                                    "NS1 variant (S283A) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         parvovirus; NADL-2 virulent strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                '*tag= a
'note= "see AAP40306"
2107, .3522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
/note= "see AAP40675"
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97.3**%;** 98.3**%**;

Local Similarity 98.3 nes 59; Conservative

Best Loc Matches

Query Match

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Gaps

. 13

Location/Qualifiers

.2073

WO8402847-A.

AAN40252 standard; DNA; 3524 BP

RESULT 7 AAN40252

Db

8

(first entry)

(revised)

24-OCT-2003 12-JAN-1992

AAN40252;

parvovirus

Porcine

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preferably derived from vB1440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pGEM3Z or pGEMSZ. The host cells to be transfected ar selected from Norden Laboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells or canine A72 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parvovirus; dog; vaccine; CPV; myocardial disease; enteric disease; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Attenuated CPV strains contg. up to 4 mutation (s) relative to control virus - useful as a veterinary vaccine against CPV disease in animals, such as wild or domestic dogs.
                                                                                                                                                                                                                                                                                                                      1 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACCAACACA
                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                Sequence 5049 BP; 1791 A; 812 C; 1029 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                              Length 5049;
                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Attenuated canine parvovirus CPV-39 passage 60 DNA
                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                              Score 42.4; DB 2;
Pred. No. 0.00023;
                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parrish CR, Gruenberg A, Carmichael LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/note= "A G or
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81.7%;
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                                                                                                                                                                                                                                                                        49; Conservative
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/note=
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                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canine parvovirus.
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                                                                                                                                                                                                                    Query Match
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AMTH53112

AMTH54

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                                                                              1656 GGACAAACAATTAGAATTGATCAAAAAGGTAAAGGAAGTAAGCAAATTGAACCAACTCCA 1715
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/note= "base 4973 is C in virulent CPV-39 (T in passage
65 attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                              (G in passage
                                                                                                                                                                                                                                                                                                                                                                                                      passage
                                                                                                                                                                                                                                                                                                                                                                                                                                               (A in passage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (T in passage
                                                           1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAACAGATTGAACCAACACCA
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (T in
                                                                                                                                                                                                                  parvovirus; CPV; attenuation; vaccine; dog; panleukopenia virus; mink enteritis virus; infection; ds.
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0
Sequence 5049 BP; 1790 A; 814 C; 1029 G; 1416 T; 0 U; 0 Other;
                     Length 5049;
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/note= "base 4307 is A in virulent CPV-39
65 attenuated virus)"
4358
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65 attenuated virus)"
4477
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/note= "base 4477 is G in virulent CPV-39
65 attenuated virus)"
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/note= "base 4889 is C in virulent CPV-39
65 attenuated virus)"
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                                         Indels
                                         11;
                    5
                    Score 42.4; DB 2;
Pred. No. 0.00023;
0; Mismatches 11
                                                                                                                                                                                                                                                                                          *tag= a
note= "NS1/NS2 coding region"
                                                                                                                                                                                                                                                                                                                      /*tag= b
/note= "VP1/VP2 coding region'
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                                                                                                                                                                                              Attenuated canine parvovirus genomic DNA.
                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                  AAT88321 standard; DNA; 5049 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US007584.
                    Query Match
Best Local Similarity 81.7%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                           .4541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carmichael LE,
                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                              *tag=
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                                                                                                                                                                                                                                                  Canine parvovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36-MAY-1997;
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                                                                                                                                                                          21-MAY-1998
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                                                                                                                                                      AAT88321;
                                                                                                                                                                                                                                                                                                                                          mutation
                                                                                                                                                                                                                                                                                                                                                                                   mutation
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                                                                                                                                                                                                                             feline
                                                                                                                                                                                                                  Canine
                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                             CDS
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A claimed virus from the 6th passage (deposited as ATCC VR 2528)

C contains all 6 mutations. The DNA from attenuated CPV strains (see also AATB8324) is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks which, in turn, can be transfected into cells to generate master stocks which, in turn, can be transfected into cells to generate product of protect against CPV disease, or more generally in cats and minks to protect against feline panleukopenia virus and mink enteritis virus. The vaccines protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), providing a long term immune response. (NB. this sequence was created by adaptation of the wild-type CPV-2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                 molecule encodes an annenuated canine parvovirus (CPV) genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAAAAAGGTTGAACCAACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
for protection against parvovirus and feline pan-leukopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "base 97 is C or T in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canine parvovirus, CPV, attenuation, vB1440, vaccine, dog, feline panleukopenia virus, mink enteritis virus, infection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5049 BP; 1788 A; 809 C; 1029 G; 1417 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42.4; DB 2; Length 5049;
Pred. No. 0.00023;
0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= \, {f f} \,
/note= "base 4881 is C in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "base 4745 is T in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= c
/note= "base 59 is G in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Attenuated canine parvovirus (vBI440) genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/note= "NS1/NS2 coding region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine parvovirus; vBI440 (ATCC VR 2489)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT88324 standard; DNA; 5049 BP
                                                                   Claim 1; Page; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 81.7%;
ses 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286. .4541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
                         virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9742972-A1
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21-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT88324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutation
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ID AATI
XX AC AATI
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DT 21-1
DT 2
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This DNA sequence comprises an attenuated virus genome derived by serial passaging (60 times) of virulent canine parvovirus (CPV) type 2b isolate passaging (60 times) of virulent canine parvovirus (CPV) type 2b isolate 23 in NHEK feline kidney host cells. The attenuated virus is designated vB1440 (AFCC VR 2489). It contains 4 mutations relative to the sequence (see AAT88320) of the control (5th passage) wild-type CPV-2b. 2 Mutations are within the hairpin formed by the 3' terminal palindrome: the mutation at nucleotide 59 introduces and A into a G-C rich region within the tip of the hairpin, disrupting the base palining in one of the 2 small internal palindromes within that sequence; the thymine at nucleotide 97 is palindrome. The DNA from attenuated CPV strains (see also AAT88321) is used for the production of infectious molecular DNA clones, which, in the palicute of infectious molecular DNA clones, which, in the curn attenuated viruses can be used in dogs as a vaccine to protect against feline panleukopenia virus and mink enteritis virus. The vaccines protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), providing a long term immune response.

(Updated on 17-0CT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                canine parvovirus DNA carrying specific attenuating mutation(s) - used as vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parvovirus; CPV; attenuation; vBI440; vaccine; dog; panleukopenia virus; mink enteritis virus; infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5049 BP; 1791 A; 812 C; 1029 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42.4; DB 2; Length 5049;
Pred. No. 0.00023;
0; Mismatches 11; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/note= "NS1/NS2 coding region"
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/note= "VP1/VP2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canine parvovirus 39 passage #5 (wild-type).
                                                                                                                                                                                              Carmichael LE, Gruenberg A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canine parvovirus; type 2b isolate 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Page 34-37; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
273. .2279
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                                                                                                                                 CORR ) CORNELL RES FOUND INC
97WO-US007584.
                                                             96US-00647655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.7%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .4541
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(first entry)
                                                                                                                                                                                                                                                                  WPI; 1998-008583/01
06-MAY-1997;
                                                                15-MAY-1996;
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21-MAY-1998
                                                                                                                                                                                                 Parrish CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT88320;
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Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells.
                                                                                                                                                                                                                                  (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the
                                                                                                                                                                                                                 a recombinant DNA construct of a plant
                                                                                                                                                                                                                                                                                                                                                      Sequence 85680 BP; 27189 A; 16414 C; 15246 G; 26711 T; 0 U; 120 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51915 ATTCCAGTTGATCAGAAAGGAATAAGCAGTAAACACAACTAATCCACA 51868
                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 85680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 ATTCGCATTGATCAAAAGGAAAAGGCAGCAACAGATTGAACCAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAC containing repeats from centromeres 1-4 #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                           proteins such as hormones, enzymes, inters
cytokines, antibodies, and growth factors
                                                                                                                                                                                                                                                                                                                                                                                .maccn 45.3%; Score 27.2;
Local Similarity 72.9%; Pred. No. 44.
les 35; Conservative 0; Mismarches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 102; Page 431-453; 1449pp; English.
                                                                                                                                                                           Claim 102; Page 763-777; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Centromere; michrosome; vector; ds.
                    Keith K;
                                                                                                                                                                                                                 present invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keith
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99US-0127409P.
99US-0134770P.
99US-0153584P.
99US-0154603P.
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                    Copenhaver G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copenhaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
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                                                         WPI; 2000-587529/55
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16-DEC-1999;
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01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-2001
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                    Preuss D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preuss D,
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF22285
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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AAF22285/c
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                              This DNA sequence comprises the genome of virulent canine parvovirus type 2b (CPV-2b) isolate 39, obtained after 5 serial passages in NLFK feline kidney host cells. Further passaging has yielded attendated virus vB1440 (ATCC VR 2489) (See AAT88124) from the 60th passage, and a claimed virus (see AAT88121) derived from the 65th passage, and a claimed virus respectively contain 4 and 6 mutations in comparison to the virulent 5th passage virus. The DNA from attenuated CPV-2b strains is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks of the virus. The trenuated viruses can be used in dogs as a vaccine to protect against cattenuated virus and mink enteritis virus. The vaccines protect galinst the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), and provide a long term immune response. (Updated on 17-0CT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1656 GGACAAACAATTAGAATTGATCAAAAGGTAAAGGAAGTAAGGAAATTGAACCAACTCCA 1715
                                                                                                                                                                                                                                Canine parvovirus DNA carrying specific attenuating mutation(s) - used as vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAAAACAGATTGAACCAACACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5049 BP; 1789 A; 813 C; 1030 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42.4; DB 2;
Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAC containing repeats from centromeres 1-4 #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                      Gruenberg A;
                                                                                                                                                                                                                                                                                                             Example 8; Page 37-40; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Centromere; michrosome; vector; ds
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AAF22299 standard; DNA; 85680 BP
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990S-0134770P.
990S-0153584P.
99US-0154603P.
                                                                                                                (CORR ) CORNELL RES FOUND INC
                                    97WO-US007584
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                                                                           96US-00647655
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                                                                                                                                                      Parrish CR, Carmichael LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 81.7
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
                                                                                                                                                                                             WPI; 1998-008583/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200055325-A2
                                    06-MAY-1997;
                                                                           15-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAR-1999;
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ð a The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant son animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors,

CHICAGO

(UYCH-) UNIV

18-MAY-1999; 13-SEP-1999; 17-SEP-1999; 16-DEC-1999;

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Gaps

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Indels

57

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 95223 BP; 27974 A; 19452 C; 19355 G; 27745 T; 0 U; 697 Other;
                                                                                       Gaps
                             Sequence 94618 BP; 29114 A; 17215 C; 17486 G; 30801 T; 0 U; 2 Other;
                                                                                                                                                42709 ATTCCTGTTGATCAGAAAGGAATAAGCAGTAAACACAATTAATCCAGA 42662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 95223;
                                                          DB 3; Length 94618;
                                                                                                                   10 ATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACCAACA 57
                                                       Score 27.2; DB 3; Length 9 Pred. No. 45; 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                               BAC containing repeats from centromeres 1-4 #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27.2; DB pred. No. 45; 0; Mismatches
cytokines, antibodies, and growth factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 102; Page 364-385; 1449pp; English
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                                                                                                                                                                                                                          AAF22282 standard; DNA; 95223 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0125219P.
99US-0127409P.
99US-0134770P.
99US-0153584P.
99US-0154603P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 72.9%;
Matches 35; Conservative
                                                        Query Match
Best Local Similarity 72.9%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copenhaver G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
16-DEC-1999;
                                                                                                                                                                                                                                                                                   20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000
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AAF22282
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Gaps

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13; Indels

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49476 ATTCCAGTTGATCAGAAAGGAATAAGCAGTAAACACAACTAATCAAGA 49523

2, 2004, 19:08:36

Search completed: June Job time : 148.25 secs

10 ATTCGCATTGATCAAAAGGAAAAGGCAGCAAAACAGATTGAACCAACA

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1 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAACAAAACAGATTGAACCAACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QUENCTH: 5049 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
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Sequence 1,
Sequence 2,
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Sequence
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                                                                                                                                          1 ggtcaagctattcgcattga.....aacagattgaaccaacaca
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. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
. /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
. /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
. /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
. /cgn2_6/ptodata/2/ina/pcTus_compage:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-647-655-1
US-08-647-655-2
US-08-947-823-1
US-08-917-913-4
US-08-817-913-6
US-08-817-913-8
US-08-817-913-9
US-08-817-913-10
US-08-817-913-11
US-08-817-913-12
US-08-817-913-13
US-08-817-913-13
US-08-817-913-15
US-08-817-913-15
US-08-817-913-15
US-08-817-913-15
US-08-817-913-15
US-08-817-913-15
US-08-817-913-15
US-08-817-913-16
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                                                                                                                                                                                             682709 seqs, 277475446 residues
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                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
                                                                                                                  US-10-069-056-15
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Match Length
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                                                                            Run on:
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0; Gaps

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Length 5049;

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Sequence 3, Appli
Sequence 1, Appli
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Sequence 2, Appli
Sequence 2, Appli
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Sequence 1, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 11, Appli
     Sequence 19, App.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08336345
Patent No. 5814510
GENERAL INFORMATION:
APPLICANT: Barrish, Colin R.
APPLICANT: Gruenberg, Allen
APPLICANT: Garmichael, Leland E.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 Avenue of the Americas
STREET: 1155 Avenue of the Americas
STATE: NW
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,345
US-08-466-248-19

US-09-751-389-3

US-09-227-357-32

US-09-257-884-1

US-09-643-990A-1

US-09-643-990A-1

US-08-956-171E-343

US-08-956-171E-343

US-09-56-171E-343

US-09-56-171E-343

US-09-56-171E-343

US-09-26-537-13

US-09-26-537-13

US-09-26-537-13

US-09-56-537-13

US-09-56-537-13

US-09-56-537-16

US-09-576-551-112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE:
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30753
REFERENCE/DOCKET NUMBER: 7937-006
TELECHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPRX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS
1656 GGACAAACAATTAGAATTGATCAAAAGGTAAAGGAAGTAAGGAAATTGAACCAACTCCA 1715
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                                                                                                                                                             APPLICANT: Carrish, Colin R.
APPLICANT: Gruenberg, Allen
APPLICANT: Gruenberg, Allen
APPLICANT: Carmichael, Leland E.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                               ZIP: 1036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,345
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30753
REFERENCE/DOCKET NUMBER: 7937-0
TELECOMONICATION INFORMATION:
TELEPAN: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPAN: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5049 base pairs
                                                                            RESULT 2
US-08-336-345-2
Sequence 2, Application US/08336345
Patent No. 5814510
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 81.7
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
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GENERAL INFORMATION:
APPLICANT: Barrish Colin R.
APPLICANT: Gramichael, Leland B.
ITILE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES: 2
CORRESPENDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STREET: 1155 Avenue of the Americas
CITY: New York
STREET: 1036-271
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/647,655
FILING DATE: On Even Date Herewith
CLASSIFICATION NUMBER: US/08/647,655
ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ATTORNEY ACTIVE ACTIVE ATTORNEY ACTIVE ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647/655
FILING DATE: On Even Date Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30,753
REFERENCE/DOCKET NUMBER: 7937-008
TELECOMMUTICATION INFORMATION:
TELEFAK: (212) 790-9090
TELEFAK: (212) 790-9090
TELEFAK: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42.4; DB 2;
Pred. No. 1.5e-05;
0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30,753
REFERENCE/DOCKET NUMBER: 793
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 70.7%;
Best Local Similarity 81.7%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 5049 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DN HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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17;

0; Mismatches

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36; Conservative
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  Matches
                                                                                                                                                  RESULT 6
                                                                                                                                                                                                                                                                                                                                                     1656 GGACAAACAATTAGAATTGATCAAAAAGGTAAAGGAAGTAAAGGAAATTGAACCAACTCCA 1715
                                                                                                                                                                                                                                                                                                                       1 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACCAACACCA
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                   Length 5049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isgouhi
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823 FILING DATE: 09-OCT-1997 CLASSIFICATION: 800
                                                                                                                                                                                                                                 Score 42.4; DB 2;
Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: Townsend and Townsend and Crew LLP
F: Two Embarcadero Center, Eighth Floor
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-0CT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-0CT-1996
ATTORNEY AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08947823
Patent No. 6114605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECONMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                                                           TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-947-823-1
                                                                                                                                                                                                                                   70.7%;
81.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51952 base pairs
5049 base pairs
                                                                                                                                                                                                                                                     Best Local Similarity 81.7
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid sTRANDEDNESS: single
                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
STREET: Two Embarcad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                        nucleic acid
EDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francis
STATE: Californis
COUNTRY: USA
ZIP: 94111-3834
                                       STRANDEDNESS:
                                                                                                    HYPOTHETICAL:
ANTI-SENSE: N
                                                                                                                                                                                        US-08-647-655-2
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-08-947-823-1
  LENGTH:
                                                                                                                                                                                                                                   Query Match
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DB 3; Length 51952;

Score 25.8; I Pred. No. 13;

43.0%;

Query Match Best Local Similarity

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                                                                                                                                                                                                            APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE 1508
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                         42427 AAGAAATTCCTAGTTGTCAACAAGTTAAAGATAGCATAAAAATTGAAGAGCAAGA 42479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
5 AAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAACAACAGATTGAACCAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2397 gaarggaaaaagaggaaaaagccccaaacagarggaaaaa 2356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 GCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24.4; DE Fred. No. 20; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                Sequence 282, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08817913
Patent No. 6184443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 287
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 73.8%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Pedersen, Rolf
APPLICANT: Lund, Marianne
APPLICANT: Okkels, Finn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLADNOT04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: BLADN
CLONE: 1317697
                                                                                                                                IS-09-023-655-282/c
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Gaps
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40.3%; Score 24.2; DB 3; Length 518;
Best Local Similarity 71.1%; Pred. No. 16;
Matches 32; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 TTTTGAAATGGATTAAAAAAAAAAAAAAAAAAAAAATAAATTGAACC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 TATTCGCATTGATCAAAAAGGAAAAGGCAGCAAACAGATTGAACC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pedersen, Rolf
APPLICANT: Dund, Marianne
APPLICANT: Lund, Marianne
APPLICANT: Lund, Marianne
APPLICANT: Lund, Marianne
APPLICANT: Marianne
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSEE: Knobbe, Martens, Olson & Bear
F: 620 Newport Center Drive 16th Floor
Newport Beach
         APPLICATION NUMBER: US/08/817,913
FILING DATE: 15-SEP-1997
CLASSIFICATION: 800
RHICR APPLICATION DATE: ROT REPLICATION NUMBER: PCT/EP95/02196
FILING DATE: 06-UN-1995
APPLICATION NUMBER: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUIO.001APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02196
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: GB941286.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,913
FILLIG DATE: 15-8EP-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08817913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM: DOS
FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: DI
ELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-817-913-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 21-OCT-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 518 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA
T. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 TATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pedersen, Rolf
APPLICANT: Lund, Marianne
APPLICANT: Lund, Marianne
APPLICANT: Okkels, Finn
APPLICANT: Kreibs, Finn
APPLICANT: Okkels, Finn
APPLICANT: Okkels, Finn
APPLICANT: Okkels, 27
CORRESPONDENCES: 27
CORRESPONDENCES: 27
CORRESPONDENCES: Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
APPLICANT: Kreiberg, Jette
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                  PILING DATE: 15-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/EP95/02196
PRILING DATE: 06-JUN-1995
APPLICATION NUMBER: GB941286.7
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAMM: Altiman, Daniel B
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUIO.001APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,913
FILING DATE: 15-5EP-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08817913
Patent No. 6184443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FELECOMMUNICATION INFORMATION: TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.3%;
Best Local Similarity 71.1%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 514 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: list MOLECULE TYPE: US-08-817-913-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
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US-08-817-913-5
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Query Match
40.3%; Score 24.2; DB 3; Length 687;
Best Local Similarity 71.1%; Pred. No. 17;
Matches 32; Conservative 0; Mismatches 13; Indels
                         174 TTTTGAAATGGATTAAAAGAAAAAAAAAAAAAAATGAATAAATTGAACC 218
9 TATTCGCATTGATCAAAAAGGAAAAGGCAGCAAACAGATTGAACC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 TATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Pedersen, Rolf
APPLICANT: Dund, Marianne
APPLICANT: Okkels, Finn
APPLICANT: Kreiberg, Jette
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Pedersen, Rolf
APPLICANT: Lund, Marianne
APPLICANT: Chels, Finn
APPLICANT: Kreiberg, Jette
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: DYOU10.001APC
TELECOMMUNICATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Fastesc Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,913
FILING DATE: 15-5EP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02196
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: 21-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                Sequence 8, Application US/08817913
Patent No. 6184443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08817913
Patent No. 6184443
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 687 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-817-913-9
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                                                                                                                                                                                                                                          40.3%; Score 24.2; DB 3; Length 631; 71.1%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                            118 TTTTGAAATGGATTAAAAAGAAAAAAAAAAAAATAAATTGAACC 162
                                                                                                                                                                                                                                                                                                                                 9 TATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACC 53
                                                                                                                                                                                                                                                                                       0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pedersen, Rolf
APPLICANT: Pedersen, Rolf
APPLICANT: Lund, Marianne
APPLICANT: Okkels, Finn
APPLICANT: Kreiberg, Jette
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOU10.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,913
FILING DATE: 15-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/EP95/02196
FILING DATE: 0-UN-1995
APPLICATION NUMBER: GB941286.7
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altenan, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 7, Application US/08817913; Patent No. 6184443
                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 674 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                              Best Local Similarity 71.1
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 71.1
Matches 32; Conservative
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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US-08-817-913-7
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15-SEP-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 TATTCGCATTGATCAAAAAGGAAAAAGGCAGCAAACAGATTGAACC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Pedersen, Rolf
APPLICANT: Dedersen, Rolf
APPLICANT: Lund
APPLICANT: Okkels, Finn
APPLICANT: Kreiberg, Jette
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Roobe, Martens, Olson & Bear
STREET: G20 Newport Center Drive 16th Floor
CITY: Newport Beach
                            CLASSIFICATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION NUMBER: PCT/EP95/02196
FILING DATE: 06-40N-1995
ATPORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 34,115
TELEPHONE: 714-760-9404
TELEPHONE: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 71.1%; Pred. No. 18;
Matches 32; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDION TYPE: DISKELLE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTEM VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,913
FILING DATE: 15-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/EP95/02196
PLING DATE: 06-UJN-1995
APPLICATION NUMBER: GB941286.7
PILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altenan, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 34,115
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08817913
Patent No. 6184443
                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-817-913-10
                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERRESTICS:
IENGTH: 758 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LECURATIONE: 714-, CTELEPHONE: 714-760-9507
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FILING DATE: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
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40.3%; Score 24.2; DB 3; Length 6:
Best Local Similarity 71.1%; Pred. No. 17;
Matches 32; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 TATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10. Application US/08817913
; Patent No. 6184443
; GENERAL INFORMATION:
APPLICANT: Pedersen, Rolf
APPLICANT: Lund, Marianne
APPLICANT: Kealberg, Finn
APPLICANT: Krealberg, Finn
APPLICANT: Krealberg, PROMOTER SEQUENCE FROM POTATO
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUIO.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTE
COMPUTER: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/817,913
FILING DATE: 15-SEP-1997
CLASSIFICATION NUMBER: PCT/EP95/02196
APPLICATION NUMBER: COS-UN-1995
APPLICATION NUMBER: GB941286.7
FILING DATE: 21-OCT-1994
ATTONNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/817,913
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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US-08-817-913-9
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SEQUENCE CHARACTERISTICS:
LENGTH: 693 base pairs
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APPLICATION NUMBER: US
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MEDIUM TYPE: Diskette
        NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                      Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
                                                                                                                                     U.S.A.
                                                                                                                 STATE: CACOUNTRY: U.S
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40.3%; Score 24.2; DB 3; Length 859;
Best Local Similarity 71.1%; Pred. No. 18;
Matches 32; Conservative 0; Mismatches 13; Indels (
                                                                                                                                                                                                           DB 3; Length 855;
                                                                                                                                                                                                                                                                                                                                         342 ITTTGAATGGATTAAAAAGAAAAAAAAAAAAATAAATTGAACC 386
                                                                                                                                                                                                        Query Match 40.3%; Score 24.2; DB 3; Length 8: Best Local Similarity 71.1%; Pred. No. 18; Matches 32; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                      9 TATTCGCATTGATCAAAAGGAAAAGGCAGCAACAGATTGAACC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Pedersen, Rolf
APPLICANT: Lund, Marianne
APPLICANT: Okkels, Finn
APPLICANT: Kreiberg, Jette
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION: 000
PRIOR APPLICATION NUMBER: PCT/EP95/02196
FILING DATE: 06-UN-1995
APPLICATION NUMBER: GB941286.7
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUIO.001APC
TELEPHONE: 714-760-9604
TELEPHONE: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION NUMBER: US/08/817,913
FILING DATE: 15-SEP-1997
CLASSIPICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/08817913
Patent No. 6184443
                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-817-913-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: DNA (genomic) US-08-817-913-12
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SEQUENCE CHARACTERISTICS:
LENGTH: 859 base pairs
                                           LENGTH: 855 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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US-08-817-913-12
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9 TATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACC 53

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346 TTTTGAAATGGATTAAAAAGAAAAAAAAAAAAAAAATAAATTGAACC 390
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Search completed: June 3, 2004, 00:56:31 Job time: 37.75 secs This Poop Rions lusotos

Appl

Sequence

Sequence 12298, A Sequence 12298, A Sequence 21855, A Sequence 39530, A Sequence 39530, A Sequence 31447, A Sequence 21447, A Sequence 21447, A Sequence 218, App Sequence 218, App Sequence 218, App Sequence 37804, A Sequence 3180, A Sequence 25, Applised Sequ

Scoring table:

Searched:

Database

Perfect score:

Sequence:

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Run on:

Sequence 1933, Ap

Sequence 203, P Sequence 3, App Sequence 32, Appl Sequence 33, Appl

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1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAACAACAGATTGAACCAACACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and applications
US-09-730-559B-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and
FILE REFERENCE: 344 702 - US
CURRENT PRILING DATE: 2003-03-27
CURRENT FILING DATE: 2003-03-27
PRIOR PAPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: Patentin version 3.0
SEQ ID NO 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA; Cisteria monocytogenes-EGD US-10-398-221-878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2779, Application US/10398221; Publication No. US20040018514A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 878, Application US/10398221
Publication No. US20040018514A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 65.0
Matches 39; Conservative
                                              417
2725
3051
211
211
945
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87749
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7.0440.7
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US-10-398-221-2779
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Sequence 1624, Ap
Sequence 32901, A
Sequence 79561, A
Sequence 24455,
Sequence 244546,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 244546,
Sequence 78, Appl
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 21932, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 878, App
                                                                                                           2, 2004, 23:14:04; Search time 141 Seconds (without alignments) 1941.275 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                             1 ggtcaagctattcgcattga.....aacagattgaaccaacacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_MBW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NBW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_NBW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NBW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_NBW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NBW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NBW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US09_NBW_PUB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_NBW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NBW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NBW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                         5991872
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-358-221-2779
US-10-359-493-32903
US-10-369-499-32903
US-10-027-632-244545
US-10-027-632-244545
US-10-027-632-244545
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US-09-822-635-3
US-10-377-097-68
                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                         2995936 seqs, 2280998010 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-822-635-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                 nucleic search, using sw model
                                                                                                                                                                                                                                           IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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960
1925
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624
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5430
10172
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Match
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122210987654321

Score

Result No.

Gaps

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Query Match
Best Local Similarity
FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                 APPLICANT: GLASER, PALLIDDE
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT PILING DATE: 2003-03-27
FRIOR APPLICATION NUMBER: PCT/FR 01/03 061
FRIOR APPLICATION NUMBER: FT 00/12 697
FRIOR FILING DATE: 2000-10-04
FRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SEQ ID NO 2779
LENGTH: 2451
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 65.0%; Pred. No. 58;
Matches 39; Conservative 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 01109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Listeria monocytogenes EGDe
US-10-398-221-2779
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TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 495 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (617) 742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Alou Sinha
APPLICANT: Alou Sinha
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICANION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 79561
LENGTH: 1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
EROGIN NO 32903
LENGTH: 960
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                                                                                                                                                            Length 495;
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Pred. No. 97;
0; Mismatches 21;
                                                                                                                                                               DB 13;
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Pred. No. 1.2e+02;
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US-10-424-599-79561
                                                                                                                                                         Query Match
42.3%; Score 25.4; D
Best Local Similarity 68.6%; Pred. No. 80;
Matches 35; Conservative 0; Mismatches
NAME/KEY: misc_feature
;
LOCATION: (B) LOCATION 1...495
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US-10-335-977-1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32903, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 64.4%;
Matches 38; Conservative
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US-10-369-493-32903
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PRIOR FILING DATE: 1999-08-09
                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-244546
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Sequence 244546, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/227, 632

CURRENT FILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-07-12

PRIOR PLILNG DATE: 2000-04-20

PRIOR PLILNG DATE: 2000-04-20

PRIOR PLILNG DATE: 2000-03-29

PRIOR PLILNG DATE: 2000-02-24

PRIOR PLILNG DATE: 1999-11-23

PRIOR PLILNG DATE: 1999-10-28

PRIOR PLILNG DATE: 1999-09-28

PRIOR PLILNG DATE: 2000-02-24

PRIOR PLILNG DATE: 2000-02-24

PRIOR PLILNG DATE: 2000-02-24

PRIOR PLILNG DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Oblymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR APPLICATION NUMBER: US 60/18,006
FRIOR APPLICATION NUMBER: US 60/18,006
FRIOR PILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-04-20
FRIOR PILING DATE: 2000-03-29
FRIOR PILING DATE: 2000-03-24
FRIOR APPLICATION NUMBER: US 60/185,218
FRIOR PILING DATE: 1999-11-23
FRIOR APPLICATION NUMBER: US 60/165,358
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR PILING DATE: 1999-09-28
FRIOR PILING DATE: 1999-09-28
FRIOR PILING DATE: 1999-09-09-09
FRIOR FILING DATE: 1999-09-09
FRIOR FILING DATE: 1999-09-09
FRIOR FILING DATE: 1999-08-09
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      21; Indels
      Mismatches
                                                                                                                                                                                                                                                                                       Sequence 244545, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
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Best Local Similarity 64.3%;
Matches 36; Conservative
      38; Conservative
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LENGTH: 624
      Matches
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TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT PAPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PILING DATE: 2000-07-12
PRIOR PLICATION NUMBER: US 60/128,006
PRIOR PLICATION NUMBER: US 60/198,676
PRIOR PLICATION NUMBER: US 60/198,676
PRIOR PLICATION NUMBER: US 60/193,483
PRIOR PLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PLICATION NUMBER: US 60/167,363
PRIOR PLING DATE: 1090-01-3
PRIOR PLING DATE: 1099-11-21
PRIOR PLING DATE: 1999-11-21
PRIOR PLING DATE: 1999-11-21
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FEASTER FEATTER FEATTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 aacctatricagriigaaccaaaaagaarraaaaaaaaaaaaacagaccaarraca 132
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                                                                                                                                                                                                                                                                                                                                                                                         Length 624;
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                                                                                                                                                                                                                                                                                                                                                                                    Score 25.2; DB 13;
Pred. No. 1e+02;
1; Mismatches 19;
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 244546
LENGTH: 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-027-632-244546
; Sequence 244546
; Publication No. US2003024075A9
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 244545, Application US/10027632
Publication No. US20030204075A9
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Best Local Similarity 64.3%;
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020111302A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-02-8
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASELEQ for Windows Version 4.0
SEQ ID NO 244546
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CURRENT APPLICATION NUMBER: US/09/728,952
CURRENT FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 101
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pplication US/09728952
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Best Local Similarity 66.7%;
Matches 36; Conservative
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Ujwal, Manusha L
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Best Local Similarity 64.3'
Matches 36; Conservative
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
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ORGANISM: Homo sapiens
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; LOCATION: (93)..(4832)
US-09-728-952-78
                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-244546
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Sequence 3, Application US/09822635; Patent No. US20010039331A1

US-09-822-635-3

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APELCONY: Nature: A Cohn J.
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PRIOR APPLICATION NUMBER: US 60/216,820
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Publication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lee, John
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B

CURRENT APPLICATION NUMBER: US 60/191,031

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-25

PRIOR PILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                     1 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACCA 54
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42.0%; Score 25.2; DB 9; Length 10172;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 36; Conservative 0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hunter, John J.
APPLICANT: Hunter, John J.
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 16836, A NOVEL HUMAN PHOSPHOLIPASE C AND TITLE OF INVENTION: USES THEREOF PILE REFERENCE: 10448-035001
CURRENT APPLICATION NUMBER: US/09/822,635
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,921
PRIOR PILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                Query Match 42.0%; Score 25.2; DB 13; Length Best Local Similarity 66.7%; Pred. No. 1.8e+02; Matches 36; Conservative 0; Mismatches 18; Indels
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; OTHER INFORMATION: n = A,T,C or G
US-09-822-635-1
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US-09-822-635-1
Sequence 1, Application US/09822635;
Patent No. US20010039331A1
GENERAL INFORMATION:
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NAME/KEY: CDS
LOCATION: (3667)...(9113)
NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
     TYPE: DNA
ORGANISM: Homo Sapiens
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; NAME/KEY: CDS
; LOCATION: (1)...(5430)
US-10-377-097-68
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Grand Applicant Milennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel E.
APPLICANT: Williamson, Mark W.
APPLICANT: Williamson, Mark W.
APPLICANT: Williamson, Mark W.
APPLICANT: Williamson, Mark W.
APPLICANT: MacBeth, Kyle J.
APPLICANT: MacBeth, Kyle J.
APPLICANT: MacBeth, Kyle J.
APPLICANT: Huncer, John J.
APPLICANT: Bandaru, Rajasekhar A.
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 60/219,028
PRIOR APPLICATION NUMBER: US 60/218,053
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-3
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LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 625, 9644, 9646, 9658, 9667,
LOCATION: 9671, 9674, 9675, 9691, 9696, 9697, 9700, 9715, 9717, 9726,
LOCATION: 9736, 9737, 9738, 9741, 9743, 9754, 9760, 9768, 9771, 9773,
LOCATION: 9782, 9784, 9800, 9844, 9921, 9939, 10171, 10172
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PRIOR APPLICATION NUMBER: US 09/892,870
PRIOR PLING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,174
PRIOR APPLICATION NUMBER: US 09/775,117
PRIOR APPLICATION NUMBER: US 09/775,117
PRIOR APPLICATION NUMBER: US 09/775,117
PRIOR PLING DATE: 2001-02-01
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PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR PILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR PILING DATE: 2000-12-21
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; Sequence 66, Application US/10377097
; Publication No. US20040033509A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Search completed: June 3, 2004, 03:14:14 Job time: 143 secs

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0 0 20 0 0				0 0 0 0 2 2 2 2 2 2 3 2 3 2 3 3 3 3 3 3		c 30 31 31 37		000. 888. 8004.4			RESULT 1 CC908309 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL	COMMENT	•
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM nucleic - nucleic search, using sw model Run on: June 2, 2004, 18:15:21 ; Search time 1499.5 Seconds (without alignments) 1194.886 Million cell undates/sec		Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 27513289 segs, 14931090276 residues Total number of hits satisfying chosen parameters: 55026578	um DB seq length: 0 um DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	EST:	4: em_estmu:* 5: em_estoy:* 6: em_estppl:* 7: em_estro:*	8: em_htc:* 9: gb_est1:* 10: gb_est2:* 11: gb_htc:*		16: em_estom:* 17: em_gss_hum:* 18: em_gss_inv:* 19: em_gss_pln:* 20: em_gss_vrt:*	em_988 em_988 em_988	25: em_gss_rod:* 26: em_gss_phg:* 27: em_gss_vrl:* 28: gb_gssl:* 29: db_gssl:*	the i	SUMMARIES . SUMMARIES	1 29 48.3 820 CC908309 CC908309 t042b20ba 2 28.4 47.3 778 28 BZ148321 BZ148321 CH230-267 C 3 28.2 47.0 466 10 BE751141 BE751141 202882 MA 4 27.8 46.3 240 12 BJ360453 BJ360453 BJ360453

Gaps

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Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith.T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Suduckenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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Library made from pooled tissue from testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
                                                                                                                                                                             429 gerchadecarrentararanahahahahaharekaharakaharraharen 482
                                                                                                                                 1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAAACAGATTGAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 466;
                                    Length 778;
                                                                                                                                                                                                                                                                                             BE751141 466 bp mRNA linear 202882 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BE751141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.0%; Score 28.2; DB 10;
ilarity 73.5%; Pred. No. 6.6e+02;
Conservative 0; Mismatches 13;
                                    Score 28.4; DB 28;
Pred. No. 5.6e+02;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adrenal, and endometrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .466
/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACKWARD: GTTTTCCCAGTCAGACG
Plate: 42 row: K column: 22
Seg primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                 BE751141.1 GI:10165133
                                         47.3%;
                                         Query Match
Best Local Similarity 70.4
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
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BE751141/c
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BJ360453
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                                                                                                                                                                                  셤
                                                                                                                                                                                  /cell_type="Blood"
/clone_lib="TAMBT"
/clone_loctor: pBeloBACI1, Site_1: HindIII; Site_2:
HindIII; TAMBT Bovine BAC library (Wale) produced by Texas
A&M University, Department of Animal Science."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BZ148321
CH230-267G24.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-267G24, genomic survey sequence.
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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Fleter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 267 row: G column: 24
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Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Rat BAC End Seguences from Library CHORI-230 Mbol segment
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Murinae;
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/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
/TORI-230 Rat (BN/SsMHsd/MCW) BAC library produced by
Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                         /organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Angus bull T A M U Shoshone Y6 11519666"
/db.xref="taxon:9913"
/clone="t042b20ba"
                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                               21
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Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               7 GCTATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAA
                                                                                                                                                                                                                                                                                                                                                     Score 29; DB 29;
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-267G24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Norway rat)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                   / Match 48.3%;
Local Similarity 77.8%;
les 35; Conservative
                                                                                                                                                                 /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seg primer: T'
Class: BAC ends.
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Gaps ö 51 3 TCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAAACAGATTGAA

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Length 435; Indels

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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                 1 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAACAACAGATTGAACCAACAC 58
                                                                                                                                                                                                                                                                                            ch 46.0%; Score 27.6; DB 28; 1 Similarity 67.2%; Pred. No. 9.7e+02; 39; Conservative 0; Mismatches 19;
                                                                                                      /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="plate=2195 Col=11 Row=B"

    .435
    /organism="Homo sapiens"

                       High quality sequence stop: 435.
Location/Qualifiers
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Canis familiaris
                                                                                                                                                                       /sex="male"
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    Class: BAC ends
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Best Local Similarity
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Matches 33; Conserv
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CE744031/c
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CD459995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ292792

HS 2195_B1_A06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=11 Row=B, genomic survey
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    EST 07-MAR-2002
BJ360453 Dictyostelium discoideum cDNA linear EST 07-MAR-20
BJ360453 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc6m05 5', mRNA sequence.
                                                                                                                         Dictyostelium discoideum
Dictyostelium discoideum
Bictyostelium discoideum
Eukaryota; Mycetczca; Dictyosteliida; Dictyostelium.
1 (bases 1 to 240)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="mat A"
/dev_stage="Culmination stage"
/clone_lib="Dictyostelium discoideum cDNA library, CF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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46.3%; Score 27.8; DB 12; Length 240;
Best Local Similarity 71.4%; Pred. No. 9.1e+02;
Matches 35; Conservative 0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAAACAGATTGAA 51
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High Throughput Sequencing Center
University of Washington
JOI Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                      Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-55-81-6856
Fax: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genee.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: jwallace@u washington.edu
Sequence Tagged Connector
Plate: 2195 row: B column: 11
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/clone="ddc6m05"
                                                                                      BJ360453.1 GI:19260048
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AQ292792.1 GI:4010585
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cb/44U31 693 bp DNA linear GSS 30-SEP-2003 tigr-gss-dog-17000330588335 Dog Library Canis familiaris genomic, genomic survey sequence.
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
TT: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. I toses I to 69. Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9815"
/clone_lib="Dog Library"
/note="Site_1: BskXI; Libraries were prepared from peripheral Dlood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 ATTCGCATTGATCAAAAGGAAAAGGCAGCAACAGATTGAA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.0%; Score 27.6; DB 29;
78.6%; Pred. No. 9.3e+02;
iive 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                    CE744031.1 GI:37084378
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Gaps

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ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

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CB179134 303 bp mRNA linear EST 31-JAN-2003 ioOlc10.xl Kaestner ngn3 wt Mus musculus cDNA 3', mRNA sequence.
CB179134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 303)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, B., Ronko, I., Bennett, J., Gradenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Cole, R., Tsagareishvili, R., Endocrine, Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611, 2000) Library was constructed by Catherine Lee DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Marie Scearce (mscearce@mail.med.upenn.edu)
Seq primer: -400P from Gibco
High quality sequence stop: 247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Other ESTs: ioOlc10.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/mol_type="mRNA"
/strain="129/Sv x CD1"
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/none "Organ: pancreas; Vector: pSPORT1 (GIBCO); Site_1:
                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4577"
/clone="zxwBMa0247220"
/clone=lb=zxw 0.7 1.5 KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

45.7%; Score 27.4; DB 28; Length 818;
Best Local Similarity 75.6%; Pred. No. 1e+03;
Matches 34; Conservative 0; Mismatches 11; Indels 0
           9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 AAGATATGAGCATTGAGCAGGAACAAAAATGCAGCAATCAGCTTG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AAGCTATTCGCATTCAAAAAGGAAAAGGCAGCAAACAGATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA"
/strain="B73"
                                                                                                                                                                                                                1. .818
/organism="Zea mays"
                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                  Seg primer: TR
Class: sheared ends.
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CB179134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stāge="Asexual"
/lab_host="E. coli DH10B"
/clone_lib="Fg09_AAFC_ECORC_Fusarium_graminearum_simple_su
bstrate
                                                                                                                                                                                                                                                                                                                                 Watson, R.J., Heys, R., Couroux, P., De Moors, A., Harris, L.J.,
Hattori, J., Lacroix, C., Masotti, M., Ouellet, T., Robert, L.S.,
Singh, J.A., Sprott, D. and Tinker, N.A.
A cDNA library prepared from Fusarium graminearum grown on a simple
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                          EST 03-JUN-2003
936 bp mRNA linear EST 03-JUN-200:
Fg09_07g13_A Fg09_AAFC_ECORC_Fusarium_graminearum_simple_substrate
Gibberella zeae cDNA clone Fg09_07g13, mRNA sequence.
CD459995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBluescript II+; Site_1: EcoR1; Site_2: XhoI; Fusarium graminearum grown on a simple substrate-minimal media supplemented with amino acids."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 818)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAACAAGATTGAACCAACAC 58
                                                                                                                                                                                            Gibberella zeae
Gibberella zeae
Eukaryota; Prugi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 936)
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Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Big. 20, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
CANADA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Gibberella zeae"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:5518"
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/tissue_type="Mycelium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: (613) 759-1655
Fax: (613) 759-1701
Email: watsonrj@agr.gc.ca.
Location/Qualifiers
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Other_GSSs: OGFBF10TC
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BZ736749.1 GI:28715835
                                                                                                                                     CD459995.1 GI:31374735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2003)
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Best Local Similarity
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VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE

AUTHORS

DEFINITION

BZ736749 RESULT 8

ACCESSION

Matches

ORIGIN

Query Match

DRIGIN

Matches

ò 셤 LOCUS DEFINITION

RESULT 10 BU558840

ACCESSION

VERSION KEYWORDS

ORGANISM

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AUTHORS TITLE JOURNAL COMMENT

REFERENCE

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AA389222 32-APR-1997
mp24AD8.rl Life Tech mouse embryo 8 5dpc 10664019 Mus musculus cDNA
clone IMAGE:570207 5' similar to gb:X65488 cds1 HETENGENOUS
NUCLEAR RIBONUCLEOPROTEIN U (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases I to 322)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xrefe="taxon:10090"
/clone="lMAGE:570207"
/clone="taxon:10090"
/drsue_trype="embryo"
/lab_host="DH10B"
/clone_lib="Life Tech mouse embryo 8 5dpc 10664019"
/note="Organ: whole embryo; Vector: pCMV-SPORT2; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. 8.5dpc embryos. pCMV-SPORT2 vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY531592 BXSIS92 RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus cDNA clone F630214M15 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
7 GCTATTCGCATTGATCAAAAGGAAAAGGCAGCAAAAAGATTGAACCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 45.0%; Score 27; DB 9; Length 322; Best Local Similarity 70.6%; Pred. No. 1.5e+03; Matches 36; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
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Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                               AA389222.1 GI:2042176
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AA389222/c
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/lab host="NHIOB (T1-phage-resistant)"
/lab host="NHIOB (T1-phage-resistant)"
/clone_lib="NTHI MGC_IT1-phage-resistant)"
/clone_lib="NTHI MGC_IT1-phage-resistant)"
/cote="Organ: Brain; Vector: pDNR-LIB; Site 1: SfiI
/note="Organ: Brain; Vector: pDNR-LIB; Site 1: SfiI
/note="Organ: Brain; Vector: pDNR-LIB; Site 1: SfiI
/note="Organ: Cote 2: SfiI (ggccgctcggc); cDNA made
by oligo-dT priming and directionally cloned. S' and 3'
adaptors were used in cloning as follows:
5'-ATCTACAGGCCGACAGGTGCCCATTACGCCGGG-3' and
5'-ATCTACAGGCCGACAGGCGCCGACATG-GT(30)Nu-3'. Full-length
enriched library was constructed using the Clontech
Creator SWART kit and size-selected to contain the 0.2-0.5
kb size fraction (other fractions present in NIH MGC_143).
Library created in the laboratory of M. Brownstein (NIMH,
NIH). Note: this is a NIH_MGC Library."
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Not I; Site 2: Sal I; The library was prepared by Catherine S. Lee and has not been published. The pancreas was obtained from Gerard Gradwoll (PNAS 97 P1607-1611, 2000). The cDNA's were prepared with an oligo containing a NotI site, and Sall linkers were added to the ends. The inserts were cut with NotI before being cloned into the NotI-Sall sites in the vectors. This is one of two libraries, ngn3 wt and ngn3 -/-. The wt library is in pSPORTI, T7 promoter is 5'."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 786)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbe-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Michael Brownstein
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2802 row: j column: 05
High quality sequence stop: 593.
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT_10337658 NIH_MGC_144 Mus musculus cDNA clone
IMAGE:6587429 5', mRNA sequence.
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Pred. No. 1.2e+03;
0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                  45.3%; Score 27.2; DB 14; Length 303; 67.9%; Pred. No. 1.3e+03;
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/db_xref="taxon:10090"
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Mus musculus
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Matches 35; Conservative (
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source

FEATURES

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Gaps

0; 57 EST 14-DEC-2002

Mus musculus

ORGANISM

9 TATTCGCATTGATCAAAAGGAAAAGGCAGCAACAACAGATTGAACCAACA 57

ORIGIN

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PREFERENCE OF A PREAR SET OF CHRISTICAL VENCHERELS, BIRELOGE CONTINUED IN THE CONTINUED IN
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Location/Qualifiers

FEATURES

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BJ341121 Bictyostelium discoideum cDNA library, AF Dictyostelium discoideum cDNA library, AF Dictyostelium discoideum cDNA clone dda5e11 3', mRNA sequence.
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                                                                                      /cell type="NOD-derived CD11c +ve dendritic cells"
/clone lib="RIKEN full-length enriched, NOD-derived CD11c
+ve dendritic cells"
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Dictyostelium discoideum
Bictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 554)
Urushihara 1 t. Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="mat A"
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/clone_lib="Dictyostelium discoideum cDNA library, AF"
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Center For Genetic Resource Information
National Institute of Genetics
National Institute of Sanctics
Till Yata, Mishima, Shizuoka 411-8540, Japan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'organism="Dictyostelium discoideum"
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Pred. No. 1.8e+03;
0; Mismatches 14;
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                                                  /db_xref="taxon:10090"
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Location/Qualifiers
              /mol_type="mRNA"
/strain="NOD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="dda5e11"
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EST.
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GSS.
Canis familiaris (dog)
                                                                                                                                                                                Query Match
Best Local Similarity 71.4%;
Matches 35; Conservative
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, asterids, lamids; Solanales, Convolvulaceae, Ipomoea.

(bases 1 to 623)

Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T., Nitasaka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S. Unpublished (2002)
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/db_xref="texon:35883"
/clone="jm31a10"
/tissue type="mixture of flower and flower bud"
/clone_lib="Ipomoea nil mixture of flower and flower bud"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BJ575778 Ipomoea nil mixture of flower and flower bud Ipomoea nil CDNA clone jm31a10 3', mRNA sequence.
BJ575778 BJ575778 BJ575778.1 GI:27257606
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. I bases 1 to 621)
Kirhess, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9615"
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/note="Site_l: BstXI; Libraries were prepared from
periphe"cal Blood"
                                                                                                                                                        The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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44.3%; Score 26.6; DB 29; Length 621;
Best Local Similarity 78.0%; Pred. No. 1.8e+03;
Matches 32; Conservative 0; Mismatches 9; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
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'pomoea nil'
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Muscovy d Muscovy d NS1 prote Parvoviru

Aae28648

Muscovy d Rep prote Rep prote

Goose par Barbaric

Aae26944 Abbu64764 Abr43402 Aay97723 Aay97723 Aae22869 Aae22864 Aae26943 Aae26943 Aae26943 Aae26943 Aae26943 Aae47762 Abbu64868 Abbu64762 Abbu64762 Abbu64763 Abbu64763

Barbarie

Goose par Goose par Barbarie Rep prote

Parvoviru Parvoviru

Goose par Barbarie Rep78 pro

Run on:

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/note= "Wild type Thr substituted with Ala; This location corresponds to position 463 of the NS1 variant (T463A) shown in AAY72710"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a peptide fragment of parvovirus non-structure protein 1 (NSI) variant (T463A). The invention relates to the variants of the parvovirus non-structure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                    NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                                                                                                                                                                    Parvovirus non-structure protein 1 (NS1) variant (T463A) peptide.
                                                                                                                                                                         ALIGNMENTS
             ABU64869
ABU64764
ABR43402
                                    AAY97723
AAY97722
AAE22889
AAE22890
AAE28646
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ABU64868
ABU64867
ABU64762
ABU64763
ABR43401
ABR43400
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N-PSDB; AAD02804.
Misc-difference
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31-MAY-2001
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Synthetic.
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                                                             (without alignments)
118.967 Million cell updates/sec
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Aay72708
Aay72708
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Aba943706
Aba943106
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Abu87915
Abu97913
Adb70942
Aac2891
                                                     May 28, 2004, 12:48:18 ; Search time 47.5 Seconds
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                          1586107 segs, 282547505 residues
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                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       - protein search, using sw model
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AAY72706
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AAY72704
AAP40306
ABU97916
ADB70945
ABU97914
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AAY97725
AAE22892
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AAE26945
ABU64870
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ABR43403
ABU97915
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ABU97913
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AAR85384
AAY97724
AAE22891
                                                                                                   GQAIRIDQKGKGSKQIEPTP 20
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Gapop 10.0 , Gapext 0.5
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geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*
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geneseqp2003bs:*
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Match
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Maximum DB
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Database

Result ò Ą.

672

(first entry)

(revised)

461 GQAIRIDQKGKGSKQIEPTP 480

Thu Jun

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The present sequence is parvovirus non-structure protein 1 (NSI) variant
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                                                                                                                                                                                                                                                                                                                                   NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                     Parvovirus non-structure protein 1 (NS1) variant (T394A)
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                                                                                                                   AAY72708 standard; protein;
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N-PSDB; AAD02803.
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                                                                                                                                                                                                                                                                                                                                                                                                             Parvovirus
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                                                                       RESULT 3
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                                                                                                                                              요
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cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                            Gaps
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                                                                                                                                         100.0%; Score 103; DB 4; Length 20; 100.0%; Pred. No. 7e-10; ive 0; Mismatches 0; Indels
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(first entry)
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                                                                                                                                                                 Local Similarity 100.
nes 20; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                               Sequence 20 AA;
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31-MAY-2001
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/note= "Wild type Thr substituted with Ala"

99EP-00115161.

Rommelaere

Location/Qualifiers

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(T394A). The invention relates to the variants of the parvovirus non-
structure protein (NSI) having a shifted equilibrium between the DNA
replication and transcription activities, and the cytotoxicity activity.
These variants are useful as toxins for treating tumoural diseases. The
variant DNAS are useful as vectors for gene therapy. (Updated on 06-AUG-
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(first entry)
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Best Local Similarity 95.0
Matches 19; Conservative
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31-MAY-2001
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Gaps

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GQAIRIDQKGKGSKQIEPTP 20

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The present sequence is a parvovirus wild-type non-structure protein 1 (NS1). The present invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytocoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                             Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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0; Mismatches
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N-PSDB; AAD02799.
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                          13-AUG-1999;
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Matches
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                                                    NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
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                                                                                                                                                                                                                                                                                   /note= "Wild type Thr substituted with Ala"
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non-structure protein 1 (NS1) variant (T363A)
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Pred. No. 1.4e-07;
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95.0%;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-212717/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 19; Consern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAD02801.
                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1077260-A1
                                                                                                                                                                                                                                                                                                                                              EP1077260-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-2003
31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2001
                                                                                                                                               Parvovirus.
                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY72702
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                                                                                             The present sequence is parvovirus non-structure protein 1 (NS1) variant (S281A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence encoded by the double-stranded replicative form DNA of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide obtd. by recombinant DNA methods - for vaccination against parvovirus infections in man and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The inventors claim an immunologically active polypeptide for the development of vaccinal immunity against parvovirus infection. Also claimed are DNA sequences wholly or partly duplicative of defined sequences. The polypeptides are used in vaccines for conferring protection against parvovirus infections in man and animals. (Updated 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                               96.1%; Score 99; DB 4; Length 672; 95.0%; Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein envelope; immunogen; vaccine; antigen; epitope
transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Table II, Page 33-49; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porcine parvovirus; NADL-2 virulent strain.
                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                  Claim 6; Page 14-16; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP40306 standard; protein; 690 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              461 GQTIRIDQKGKGSKQIEPTP 480
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84WO-US000063
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84US-00567968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                   2003 to correct OS field.
                                                                                                                                                                                                                                                                                                                                                                Local Similarity 95.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1984-201354/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAN40252
                                                                                                                                                                                                                                                                                                 Sequence 672 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JAN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JAN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JAN-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO8402847-A
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12-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-AUG-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP40306;
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fox GM;
                                                                                                                                                                                                                                                                                                                                                                                               Matches
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AAP40306

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The present invention relates to method for producing peptides, polypeptides, or proteins having a predetermined property. The method compisions of a producing a population of sets of polymucleotide sequences that encode modified forms of a target protein, (b) introducing each set of polymucleotide sequences into host cells and expressing the encoded protein, where the host cells are present in an addressable array, and contein, where the host cells are present in an addressable array, and protein, where the host cells are present in an addressable array, and contein, where the host cells are present in an addressable array, and proteins, particularly those that act in complex biological settings, by rational miteagenesis. The method is also used for generating protein variants and for titering viruses. ABU97391-ABU97952 represent Adeno associated virus (AAV) mutant rep proteins used as an exemplification of the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at the vipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing proteins with a predetermined property comprises introducing nucleic acids encoding a modified target protein into host cells and expressing and screening for proteins with different activity than the target protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide production; protein production; target protein;
high throughput directed evolution; rational mutagenesis; AAV;
protein variant generation; virus titering; Adeno associated virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Adeno associated virus (AAV) mutant rep protein #526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 526; 141pp; English.
                                                                                                                                                                                        ABU97916 standard; protein; 312 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flaux M;
464 GQTIRIDQKGKGSKQIEPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-2001; 2001US-0315382P.
17-DEC-2001; 2001US-00022249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-AUG-2002; 2002WO-IB003921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rep protein; mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NAUT-) NAUTILUS BIOTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adeno associated virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vega M, Drittanti L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-354538/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003023032-A2.
                                                                                                                                                                                                                                                                                                                                          30-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                             ABU97916;
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Matches
                                                                                                                                                     ABU97916
                                                                                                           RESULT
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96.1%; Score 99; DB 1; Length 690; 95.0%; Pred. No. 1.4e-07; ive 0; Mismatches 1; Indels

19; Conservative

Query Match Best Local Similarity Matches 19; Conserv

ADB70945 standard; protein; 312 AA.

RESULT 9 ADB70945 (first entry)

04-DEC-2003

ADB70945;

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The present invention relates to method for producing peptides, polypeptides, or proteins having a predetermined property. The method compariess (a) producing a population of sets of polymuclectide sequences that encode modified forms of a target protein, (b) introducing each set of polymuclectide sequences into host cells and expressing the encoded protein, where the host cells are present in an addressable array, and protein, where the host cells are present in an addressable array, and protein, where the host cells are present in an addressable array, and protein, performing high throughput directed evolution of peptides and proteins, particularly those that act in complex biological settings, by raziants and for titering viruses. ABU97391-ABU97952 represent Adeno associated virus (AAV) mutant rep proteins used as an exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in clearny twips. The muthod is clectronic format directly from WIPO at the vibo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                        Producing proteins with a predetermined property comprises introducing nucleic acids encoding a modified target protein into host cells and expressing and screening for proteins with different activity than the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutant; mutein; adeno-associated virus; AAV; anti-HIV; gene therapy; Rep 78; human papilloma virus; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.9%; Score 72; DB 6; Length 397; 65.0%; Pred. No. 0.0024; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adeno-associated virus Rep mutant SEQ ID NO:524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 524; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB70943 standard; protein; 397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 GSAVRVDQKCKSSAQIDPTP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                     Flaux M;
                                                                                            16-AUG-2002; 2002WO-IB003921
                                                                                                                                    27-AUG-2001; 2001US-0315382P.
17-DEC-2001; 2001US-00022249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-AUG-2002; 2002WO-IB004087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-2001; 2001US-0315382P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 65.0
Matches 13; Conservative
                                                                                                                                                                                                         (NAUT-) NAUTILUS BIOTECH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
Adeno-associated virus.
                                                                                                                                                                                                                                                     Vega M, Drittanti L,
                                                                                                                                                                                                                                                                                                  WPI; 2003-354538/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 397 AA;
WO2003023032-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003018820-A2
                                                                                                                                                                                                                                                                                                                                                                                                                    target protein.
                                            20-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
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  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel adeno-associated virus (AAV), comprising an uncleic acid encoding the sequence comprising 19-621 amino acids, given in the specification. A virus of the invention has anti-HIV activity, and may have a use in gene therapy. The protein used in the invention is Rep Ps protein. The AAV is useful for preparing a composition for treating or inhibiting human papilloma virus or HIV infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                              mutant; mutein; adeno-associated virus; AAV; anti-HIV; gene therapy; Rep 78; human papilloma virus; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptide production; protein production; target protein; high throughput directed evolution; rational mutagenesis; AAV; protein variant generation; virus titering; Adeno associated virus; rep protein; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New adeno-associated virus, useful for preparing a composition for treating or inhibiting human papilloma virus or HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.9%; Score 72; DB 7; Length 312
65.0%; Pred. No. 0.0018;
ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adeno associated virus (AAV) mutant rep protein #524.
                                                                                                                                                                                 Adeno-associated virus Rep mutant SEQ ID NO:526
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Claim 21; SEQ ID NO 526; 869pp; English

Drittanti L, Flaux M;

Vega M,

WPI; 2003-278671/27

(NAUT-) NAUTILUS BIOTECH

SX C C C C C C C X SX X B X B X B

16-AUG-2002; 2002WO-IB004087. 27-AUG-2001; 2001US-0315382P. 17-DEC-2001; 2001US-00022390.

Adeno-associated virus.

Synthetic

WO2003018820-A2.

36-MAR-2003

ABU97914 standard; protein; 397 AA

(first entry)

30-JUL-2003

ABU97914;

Adeno associated virus. Synthetic.

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Query Match Best Local Similarity 65.0 Matches 13; Conservative

Sequence 312 AA;

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Gaps

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a nucleic acid encoding the sequence comprising 19-621 amino acids, given in the specification. A virus of the invention has anti-HIV activity, and may have a use in gene therapy. The protein used in the invention is Rep 78 protein. The Apvisi useful for preparing a composition for treating or inhibiting human papilloma virus or HIV infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New library of fusion nucleic acids each encoding a Rep protein recognized by a nucleic acid modification enzyme and a candidate protein, useful for detecting protein-protein interactions, protein drug discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion nucleic acid library; Rep protein; tumour cell; apoptosis; nucleic acid modification enzyme; cell death; decreased cell growth; protein-protein interaction detection; cell division; cancer therapy;
                                                                                                                New adeno-associated virus, useful for preparing a composition for treating or inhibiting human papilloma virus or HIV infection.
                                                                                                                                                                                    The invention relates to a novel adeno-associated virus (AAV),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein drug discovery; pharmacogenetics; NS1 protein
                                                                                                                                                                                                                                                                                                                                             0.0024;
                                                                                                                                                                                                                                                                                                                               69.9%; Score 72; DB 7; 65.0%; Pred. No. 0.0024;
                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE,
                                                                                                                                                         Claim 21; SEQ ID NO 524; 869pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 31; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY97725 standard; protein; 461 AA
                                                                                                                                                                                                                                                                                                                                                                                                       1 GOAIRIDQKGKGSKQIEPTP 20
                                                       Drittanti L, 'Flaux M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0150004P.
17-DEC-2001; 2001US-00022390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                             13; Conservative
                          (NAUT-) NAUTILUS BIOTECH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-218443/22
                                                                                  WPI; 2003-278671/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or pharmacogenetics
                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goose parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAA91315
                                                                                                                                                                                                                                                                                                       Sequence 397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200114539-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY97725;
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                       Vega M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li M;
                                                                                                                                                                                                                                                                                                                                                               Matches
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to a library of fusion nucleic acids, each encoding a Rep protein, a candidate protein, a presentation structure, a targeting sequence or a clabel. The Rep protein is a nucleic acid modification enzyme. The random or directed libraries (including the CDNA libraries) can be introduced into any tumour cell, and peptides identified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The methods and compositions may also be used to detect protein protein interactions, protein drug discovery, particularly for protein drugs that interact with targets on cell surfaces, to discover DNA or nucleic acid binding proteins, using nucleic acids as targets, to screen for nucleic acid modification enzymes with decreased toxicity for the host cells, to identify or generate Rep proteins with decreased toxicity, improved caryme attachment sequences for use in expression vectors and in commandation calls. The method is useful in cancer therapy and in the commandation of the companied with other cancer therapeutics (drugs or radiation) to sensitize cells and thus induce therapeutics (drugs or radiation) to sensitize cells and thus induce care conference co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid/protein conjugate; NAP; nucleic acid modification; NAM; EAS; enzyme attachment sequence; cancer therapy; protein-protein interaction; drug discovery; NS1 protein; gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library of nucleic acid/protein conjugates, has a fusion of nucleic acid modification enzyme and candidate compound, and expression vector having a fusion of nucleic acids encoding NAM enzyme and the compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to genetic libraries of nucleic acid/
protein (NAP) conjugates comprising a fusion polypeptide (with a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.9%; Score 72; DB 4; larity 70.0%; Pred. No. 0.0028; Conservative 2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Encoded by ATT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 GSAVRVDQKCKGSVCIEPTP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE22892 standard; protein; 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goose parvovirus NS1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-2001; 2001WO-US028702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-2000; 2000US-0232960P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
ses 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li M, Melander C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (XENC-) XENCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goose parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD36286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 461 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200222826-A2
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Matches
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Gaps

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Length 397; 4; Indels

acid modification (NAM) enzyme (E) and candidate compound), an expression vector (with a fusion of nucleic acids encoding the enzyme and candidate protein respectively), an enzyme attachment sequence (RAS; RNA sequence), where the candidate compound and candidate protein are different and BAS and the enzyme are covalently linked. The NAP conjugates are useful in screens to assay binding to target molecules and/or to screen candidate agents for the ability to modulate the activity of the target molecule. They are useful in cancer therapy. Sequences of the invention are also useful to detect protein-protein interaction, in drug discovery, to discover DNA or nucleic acid binding proteins, using nucleic acids as the targets and to screen for NAM enzymes with decreased toxicity for host cargets and to screen for NAM enzymes with reduced toxicity). NAP conjugates calls (specifically Rep proteins with reduced toxicity). NAP conjugates calls useful in pharmacogenomic studies, for screening bioactive agents on surface cells, viruses and microbial organisms. They are also useful for screening proteins causing phenotypic changes such as construction or inhibition of protein expression, or proteins that alter attachment, infectivity, etc. of the virus. Sequences of the invention are also used in gene therapy. The present sequence is Goose construction are also used in the invention 

Sequence 461 AA;

69.9%; Score 72; DB 5; Length 461; 70.0%; Pred. No. 0.0028; ive 2; Mismatches 4; Indels 232 GSAVRVDOKCKGSVCIEPTP 251 1 GOAIRIDOKGKGSKOIEPTP 20 Local Similarity 70.0 es 14; Conservative Query Match Matches g ઢ

RESULT 14

AAE28649 standard; protein; 461 AA

AAE28649;

(first entry) 27-DEC-2002

Goose parvovirus NS1 protein.

Nucleic acid modification enzyme; NAM; enzyme attachment sequence; EAS; protein design automation; PDA; cancer; protein-protein interaction; infection; gene therapy; NSI protein.

parvovirus Goose

WO200268453-A2.

06-SEP-2002.

19-FEB-2002; 2002WO-US004853.

22-FEB-2001; 2001US-00792629.

(XENC-) XENCOR INC.

Li M, Dahiyat BI;

WPI; 2002-691653/74. N-PSDB; AAD46143 Generating a library of fusion nucleic acids for treating cancer or infection, or detecting protein-protein interaction, comprises providing computationally-derived library of candidate protein sequences and expression vectors.

Disclosure, Page 199-201; 246pp; English.

The present invention relates to a novel method of generating a library of fusion nucleic acids. The method involves providing a computationally-derived library of candidate protein sequences and creating a library of expression vectors containing a fusion nucleic acid having a sequence 

a candidate protein sequence from the library and an enzyme attachment sequence (EAS) that is recognised by the NAM enzyme. The invention also relates to the use of a variety of computation methods including protein design automation (PDA). The method is useful in generating and screening fusion nucleic acids that may be used in treating cancer or infections, in detecting protein interactions, discovery of DNA or nucleic acids in protein interactions, screening for nucleic with decreased toxicity to the host cells and NAM enzyme/EAS pairs with increased affinity or in pharmacogenetic studies. The invention is also used in gene therapy. The present sequence is goose parvovirus NS1 protein. This sequence is used to illustrate the method of the invention encoding a nucleic acid modification (NAM) enzyme and a sequence encoding 

Sequence 461 AA;

Gaps ; 0 69.9%; Score 72; DB 5; Length 461; 70.0%; Pred. No. 0.0028; ive 2; Mismatches 4; Indels Local Similarity 70.0 les 14; Conservative Query Match Best Loca Matches

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232 GSAVRVDQKCKGSVCIEPTP 251 1 GOAIRIDOKGKGSKOIEPTP 20 ઠે 셤

RESULT 15

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Gaps ; 0 AAE26945 standard; protein; 461 AA.

AAE26945;

13-DEC-2002 (first entry)

Goose parvovirus NS1 protein.

Prokaryotic library, candidate protein; nucleic acid modification; NAM; enzyme attachment sequence; BAS; clinical pharmacology; chemical sensor; enzymology; cosmetic research; toxic; environmental safety assessment; nutrient biology; NS1. 

Goose parvovirus.

WO200266653-A2.

29-AUG-2002

14-DEC-2001; 2001WO-US049058.

14-DEC-2000; 2000US-0256163P

(XENC-) XENCOR INC

Liu Y; Li M, WPI; 2002-667068/71. N-PSDB; AAD44605 New library of prokaryotic pET-24a expression vectors, host cells or nucleic acid/protein conjugates, useful for screening candidate proteins and their nucleic acids or modification enzymes for pharmacogenetic analysis

Disclosure, Fig 31; 127pp; English.

The invention relates to methods and compositions for the construction of prokaryotic libraries expressing candidate proteins and the use of these libraries to identify candidate proteins and the nucleic acids encoding them. The invention provides a library of prokaryotic pET-24a vectors comprising a fusion nucleic acid consisting of a nucleic acid encoding a nucleic acid modification (NAM) enzyme or a candidate protein, or a nucleic acid acid arming a Ty promoter operably linked to the NAM enzyme or the candidate protein, and an enzyme attachment sequence (EAS) recognised by the NAM enzyme. The library is used for identifying candidate proteins and nucleic acids encoding these proteins, in screening for NAM enzymes

with decreased toxicity for the host cells, or in identifying novel or improved EASs, which may be used for understanding cellular processes or any subsequent thrarapeutic or toxic activities. The nucleic acid/protein (NAP) conjugates are useful in diagnostic assays and in research including clinical pharmacology, functional genomics, pharmacogenomics, agricultural chemicals, environmental safety assessment, chemical sensor, nutrient biology, cosmetic research or enzymology. These may also be used in in vitro screening techniques and in assays with target molecules. The present sequence is Goose parvovirus NSI protein used in the invention 88888888888

Sequence 461 AA;

0; Gaps Ouery Match 69.9%; Score 72; DB 5; Length 461; Best Local Similarity 70.0%; Pred. No. 0.0028; Matches 14; Conservative 2; Mismatches 4; Indels

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Search completed: May 28, 2004, 12:57:05 Job time : 48.5 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                    Copyright
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- protein search, using sw model OM protein May 28, 2004, 12:52:43 ; Search time 10.5 Seconds Run on:

(without alignments) 183.222 Million cell updates/sec

US-10-069-056-17

103 1 GQAIRIDQKGKGSKQIEPTP 20 Perfect score:

Scoring table:

Sequence:

BLOSUM62 Gapext 0.5

283366 segs, 96191526 residues Searched:

283366 of hits satisfying chosen parameters: Total number

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR 78:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	noncapsid protein	noncapsid protein	ש		ש							noncapsid protein		hypothetical prote	hisA protein - Cor	probable type II D	noncapsid protein	hypothetical prote	acriflavin resista	transcription regu	probable transcrip	insertion element	insertion element	probable insertion	probable transposa	hypothetical prote	ATP-binding transp	pectin methylester	amino acid transpo
SUMMARIES	ΙD	UYPV1F	UYPVPP	UYPVNA	A44276	UYPVCP	UYPVME	UYPVFP	UYPVV1	UYPV1M	UYPVIM	852209	UYADIA	AC0358	S77377	JE0213	G72659	UYPV19	T00382	AD3557	AI2997	H98285	H81802	F81855	E81858	H81889	AE3118	B98169	T04359	S38111
	ength DB	392 1	660 1	662 1	668 1	668 1	668 1	9	672 1	672 1	721 1	626 2	536 1	259 2	225 2	245 2				364 2	-		•		273 2			346 2	563 2	602 1
de	Query Match Length	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	6.69	65.0	46.6	44.7	44.7	44.7	44.7	44.2	43.7	43.2	43.2	42.7	42.7	42.7	42.7	42.7	42.7	42.7	42.7
	Score	66	66	66	66	66	66	66	66	66	66	72	67	48	46	46	46	46	45.5	45	44.5	44.5	44	44	44	44	44	44	44	44
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penicillin-binding noncapsid protein	cold-inducible RNA	hypothetical prote	amidophosphoribosy	protein ZK1127.7 [	hemolysin (importe	IS1106 transposase	hypothetical_prote	site-specific DNA-	NADH2 dehydrogenas	DNA topoisomerase	multidrug resistan	fibronectin - chic	vitellogenin precu	probable pectinest
S49570 UYPVAD	JC6571	S09825	A70401	C88196	AI0452	G81072	AB2112	S07792	A45456	AH2134	JC5667	A29355	JC4956	C84603
7 7	~	~	N	N	~	N	7	н	N	7	Н	N	~	7
645 849	163	217	465	816	1635	335	370	424	673	727	946	1020	1659	352
42.7	41.7	41.7	41.7	41.7	41.3	40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.3
	43 41.7	43 41.7	43 41.7	43 41.7	42.5 41.3		42 40.8		42 40.8		42 40.8	42 40.8	42 40.8	41.5 40.3

# ALIGNMENTS

T 1	Ŀ
ESUL	LVQY

noncapsid protein NS1 - feline panleukopenia virus (fragment) C;Species: feline panleukopenia virus, FPLV C;Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 16-Jul-1999

C;Accession: A03697
R;Carlson, J.; Rushlow, K.; Maxwell, I.; Maxwell, F.; Winston, S.; Hahn, W.
J. Vixol. 55, 574-587, 1985
A;Title: Cloning and sequence of DNA encoding structural proteins of the autonomous parv
A;Reference number: A03697; MUID:85265017; PMID:2991581

A; Molecule type: DNA

A; Residues: 1-392 <CAR>

A;Cross-references: EMBL:M10824; NID:g333474; PIDN:AAA47160.1; PID:g333475 C;Superfamily: parvovirus noncapsid protein C;Keywords: noncapsid protein

Gaps ö Length 392; 1; Indels DB 1; 3e-08; Pred. No. 3e-C 0; Mismatches Score 99; Pred. No. Query Match
Best Local Similarity 95.0%;
Matches 19; Conservative

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# 1 GOAIRIDOKGKGSKOIEPTP 20 ઠે ď

186 GÓTÍRIDÓKGKGSKÓIEPTP 205

noncapsid protein NS1 - porcine parvovirus (strain NADL-2)
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Species: porcine parvovirus: Diaz-Aroca, E.; Casal, J.I.
R;Ranz, A.I.; Manclus, J.J.; Diaz-Aroca, E.; Casal, J.I.
J. Gen. Virol. 70, 2541-2553, 1989
A;Title: Porcine parvovirus: DNA sequence and genome organization.
A;Reference number: A33302; MUID:90010964; PMID:2794971

A; Molecule type: DNA A; Accession: A33302

A; Residues: 1-660 <RAN>

A; Cross-references: Embl.: D00623; NID:g303754; PIDN:BAA00501.1; PID:g222358
R; Vasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W.
Virology 178, 611-616, 1990
A; Fittle: The complete nucleotide sequence of an infectious clone of porcine parvovirus, A; Reference number: A36217; MUID:91021005; PMID:2219713

A; Molecule type: DNA A; Residues: 1.85, 78, 87-273, 78, 275-375, 70, 377-620, NLH', 623-624, PTPPD', 630, AIR', 634, A; Cross-references: EMBL:M38367; NID:g332987; PIDN:AAA46920.1; PID:g332989 C; Superfamily: parvovirus noncapsid protein C; Keywords: noncapsid protein

Query Match

96.1%; Score 99; DB 1; Length 660;

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R.Kariatsumari, T.; Horiuchi, M.; Hama, E.; Yaguchi, K.; Ishigurio, N.; Goto, H.; Shinage J. Gen. Virol. 72, 867-875, 1991
A;Title: Construction and nucleotide sequence analysis of an infectious DNA clone of the A;Reference number: A38350; MUID:91202123; PMID:2016597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Martyn, J.C.; Davidson, B.E.; Studdert, M.J.
J. Gen. Vizol. 71, 2747-2753, 1990
A;Title: Nucleotide sequence of feline panleukopenia virus: comparison with canine parvox A;Reference number: A36608; MUID:91073139; PMID:2174965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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C;Species: feline panleukopenia virus, FPLV
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     noncapsid protein NS1 - mink enteritis virus (strain Abashiri)
C,Species: mink enteritis virus, MEV
C,Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
                                             noncapsid protein NS1 - canine parvovirus (strain N)
C;Species: canine parvovirus, CPV
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: A29662
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                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:M19296; NID:g333438; PIDN:AAA67459.1; PID:g333439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                        canine parvovirus
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A,Residues: 1-668 «KAR»
A,Cross-reces GB:D00765; NID:g222435; PIDN:BAA00662.1; PID:g222436
C,Superfamily: parvolirus noncapsid protein
C,Keywords: noncapsid protein
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A;Cross-references: GB:X55115; NID:g60863; PIDN:CAA38910.1; PID:g60864
C;Superfamily: parvovirus noncapsid protein
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Pred. No. 5.2e-08;
0; Mismatches 1; Indels
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                                                                                                                                                            RiRed, A.P.; Jones, E.V.; Miller, T.J.
J. Virol. 62, 266-276, 1988
A;Title: Nuclectide sequence and genome organization of A;Reference number: A29962; MUID:88062992; PMID:2824850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 96.1%; Score 99; DB 1; I Best Local Similarity 95.0%; Pred. No. 5.2e-08; Matches 19; Conservative 0; Mismatches 1;
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Pred. No. 5.2e-08;
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95.0%;
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Matches 19; Conserv
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A;Residues: 1-668 <REE>
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                                                                                                                                                                                                                                                                      noncapsid protein NS1 - porcine parvovirus (strain NADL-2) (version 2)
N;Alternate names: nonstructural protein NS-1
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Accession: A36217; A46472; A33743
C;Accession: A36217; A46472; A33743
R;Vasudevacharya, J; Basak, S; Srinivas, R.V.; Compans, R.W.
Virology 178, 611-616, 1990
A;Title: The complete nucleotide sequence of an infectious clone of porcine parvovirus, A;Reference number: A36217; MUID:91021005; PMID:2219713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Bergeron, J.; Menezes, J.; Tijssen, P.
Virology 197, 86-98, 1993
A;Title: Genomic organization and mapping of transcription and translation products of
A;Reference number: A48472; MUID:94025614; PMID:8212598
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C;Species: parvovirus LullI
C;Species: parvovirus LullI
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 26-Feb-1999
C;Accession: A44276
C;Accession: A44276
R;Diffoot, N.; Chen, K.C.; Bates, R.C.; Lederma, M.
R;Diffoot, N.; Chen, K.C.; Bates, R.C.; Lederma, M.
A;Title: The complete nucleotide sequence of parvovirus LullI and localizati
A;Reference number: A44276; MUD:93297126; PMID:8517025
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A;Reaidues: 1-662 <VAS>
A;Cross-references: EMBL:M38367; NID:g332987; PIDN:AAA46920.1; PID:g332989
A;Experimental source: strain_NADL-2
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A;Residues: 1-662 <BER>
A;Experimental source: strain NADL-2, ATCC VR-742
A;Hote: sequence extracted from NCBI backbone (NCBIN:138789, NCBIP:138790)
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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Pred. No. 5.2e-08;
0; Mismatches 1;
Best Local Similarity 95.0%; Pred. No. 5.1e-08; Matches 19; Conservative 0; Mismatches 1
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A,Residues: 1-668 <DIF>
A,Cross-references: GB:M81888
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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                                                                                                               460 GQTIRIDQKGKGSKQIEPTP 479
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A;Status: translation not shown
A;Molecule type: DNA
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J. Virol. 57, 656-669, 1986
Afritle: DNA sequence of the lymphotropic variant of minute virus of mice, MVM(i), and c A, Reference number: A29510; MUID:86115415; PMID:3502703
A, Accession: A29510
A, Molecule type: DNA
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N;Contains: noncapsid protein NS2
C;Species: adeno-associated virus type 2
C;Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 16-Jul-1999
C;Accession: A03694
R;Srivastava, A.; Luuby, E.W.; Berns, K.I.
R;Srivastava, A.; Luuby, E.W.; Berns, K.I.
A;Title: Nucleotide sequence and organization of the adeno-associated virus 2 genome. A;Reference number: A03694; MUID:83164299; PMID:6300419
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N;Alternate names: nonstructural protein NS1; NS1 protein
C.Species: muscovy duck parvovirus
C.Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
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A;Cross-references: EMBL:X75093; NID:g609091; PIDN:CAA52983.1; PID:g609092
A;Experimental source: strain FM
                                                                                                                                                                                                   A;Residues: 1-645,'I',647-721 <AST>
A;Residues: 1-645,'I',647-721 <AST>
CYCOSS-references: EMBL:M12032, NID:g332289; PIDN:AAA69566.1; PID:g825477
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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F;225-536/Product: noncapsid protein NS2 #status predicted <NS2>
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C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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Matches 12; Conservative
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A; Residues: 1-536 <SRI>
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                                                                                                                                                                                                                                                                        noncapsid protein NS1 - parvovirus H1
C;Species: parvovirus H1
A;Note: host Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 16-Jul-1999
C;Accession: A03695
R;Rhode III, S.L.; Paradiso, P.R.
J. virol. 45, 173-184, 1983
A;Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybri A;Reference number: A03695; MUID:83112183; PMID:6823009
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A;Cross-references: EMBL:X01457; NID:g60993; PIDN:CAA25689.1; PID:g60994; EMBL:J02198
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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C;Species: minute virus of mice, murine parvovirus
C;Species: minute virus of mice, murine parvovirus
C;Accession: A03696
C;Accession: A03696
C;Accession: A03696
C;Accession: A03696
C;Accession: A03696
C;Accession: A03696
A;Title: The complete DNA sequence of minute virus of mice, an autonomous parvovirus.
A;Reference number: A03696; MUD:83143341; PMID:6298737
A;Accession: A03696; MUD:83143341; PMID:6298737
A;Residues: 1-672 <AST>
A;Residues: 1-672 <AST>
C;Superfemely: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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R,Astell, C.R.; Gardiner, E.M.; Tattersall, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461 GQTIRIDQKGKGSKQIEPTP 480
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                                                462 GOTIRIDOKGKGSKOIEPTP 481
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A; Residues: 1-721 <SAH>
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Search completed: May 28, 2004, 13:00:59
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                                                                                                                                                                                                                             C;Species: Yersinia peetis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001
R;Parchill, J: Wren
R;Parchill, J: Wren
C; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 02-Nov-2001
C; Accession: 377377
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; R; Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystie
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A, Cross-references: EMBL. 190906, GB: AB001339; NID: g1652492; PIDN: BAA17480.1; PID: d101821
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Superfamily: stationary-phase survival protein SurE
                                                                                                                                                                                                       chaperone protein YPO2944 [imported] - Yersinia pestis (strain CO92)
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A;Cross-references: GB:AL590842; PIDN:CAC92190.1; PID:g15980902; GSPDB:GN00175
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hisA protein - Corynebacterium glutamicum
C;Species: Corynebacterium glutamicum
C;Date: 1-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 16-Jul-1999
C;Accession: JE0213
R;Jung, S.I.; Han, M.S.; Kwon, J.; Cheon, C.I.; Min, K.H.; Lee, M.S.
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A;Accession: S77377
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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Pred. No. 4.1;
3; Mismatches
                            396 GSKVRVDQKCKSSAQIDPTP 415
20
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C;Superfamily: chaperone protein papD
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GOAIRIDOKGKGSKOIEPTP
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Best Local Similarity 57.1%;
Matches 8; Conservative
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169 NOKGRGVKVVNPTP 182
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Matches 8; Conserva
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A;Molecule type: DNA
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Biochem. Biophys. Res. Commun. 247, 741-745, 1998

A; Fitle: Cloning of the histidine biosynthetic genes of Corynebacterium glutamicum: Orgar A; Reference number: JE0213; MUID:98321198; PMID:9647764

A; Reference number: JE0213

A; Molecule type: DNA
A; Residuaes: 1-245 < JUNA
A; Residuaes:
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GenCore version 5.1.6
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OM protein - protein search, using sw model Run on:

May 28, 2004, 12:48:53 ; Search time 6.75 Seconds (without alignments) . 154.282 Million cell updates/sec

US-10-069-056-17 103 , I GOAIRIDQKGKGSKQIEPTP 20

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMARTES

					SUMMARIES	
Tribod		4				
No.	Score	Match	Leng	DB		Description
-	66	96.1	392	-	VNCS FPV	31 feline
7	66	96.1	099	Н	VNCS_PAVPN	7 porcine
٣	66	96.1	662	-	VNCS PAVPK	P52502 porcine par
4	66	96.1	668	Н	VNCS_FPV19	~
2	66	96.1	899	Н	VNCS MEVA	8
9	66	96.1	899	Н	VNCS_PAVCN	
7	66	96.1	899	-	VNCS PAVL3	
80	66	96.1	672	Н	VNCS_MUMIM	0
6	66	96.1	672	Н	VNCS_MUMIV	P03134 murine minu
10	66	96.1	672	-	VNCS_PAVHH	m
11	67	65.0	536	-1	VNCA_AAV2	
12	46	44.7	225	-	YES9_SYNY3	
13	46	44.7	246	٦	HIS4_COREF	Q8fnz7 corynebacte
14	46	44.7	246	ч	HIS4_CORGL	068602 corynebacte
15	46	44.7	385	-	TP6A_AERPE	O9ye67 aeropyrum p
16	46	44.7	671	Н	VNCS_PAVHB	
17	44	42.7		Н		
18	44	42.7		г		Q8dhn4 s arginine
19	44	42.7		П		
20	44	42.7	645	٦	SP5D_BACSU	4 bacill
21	44	42.7	805	г	VNCS_AEDEB	aedes
22	44	42.7	849	٦	VNCS AEDEV	
23	43	41.7	163	٦	CIRP_XENLA	xeno
24	43	41.7	172	٦	CIRP_HUMAN	_
25	43	41.7	172	-	CIRP MOUSE	3 111118 1
26	43	41.7	217	٦	UL62_HCMVA	
27	43	41.7	1436	-1	MRP5 MOUSE	Q9rlx5 mus musculu
28	43	41.7	1436	-	MRP5_RAT	_
29	42	40.8	370	-	EGC1 ANASP	-
30	42	40.8	387	Н	TP6A_SULTO	_
31	42	40.8	424	-	MTB1_BACSH	
32	42	40.8	628	Н	1	Q98jb6 rhizobium l
33	42	40.8	672	Н	NQO3_PARDE	P29915 paracoccus

660 AA.

PRT;

RESULT 2 VNCS\_PAVPN ID \_VNCS\_PAVPN STANDARD; AC P18547; P22965;

P11722 gallus gall 015440 homo sapien 09503 oncorbynchu 08td26 homo sapien 08td26 homo sapien P13976 escherichia 000840 neisseria m P20665 moraxella b P19257 moraxella l P34879 shiggala so 005208 sulfolobus 023670 caenorhabdi 09v0d2 pyrococcus
FINC CHICK MRP5 HUMAN VIT ONCMY CHD5 HUMAN PENK_ECOLI TRA6 NEIMB PIV MORLA MTS2 SHISO PIV MORLA MTS2 SHISO TP6A SULSH TOP2 CABEL R15E PYRAB
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# ALIGNMENTS

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                                                                                                                                                                                                                              J. Virol. 70:2508-2515(1996).
--- FUNCTION: Seems necessary for viral DNA replication.
--- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                        Bergeron J., Hebert B., Tijssen P.; "Genome organization of the Kresse strain of porcine parvovirus: identification of the allotropic determinant and comparison with those of NADL-2 and field isolates.";
                            ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01057; Parvo_NS1; T. Nonstructural protein; DNA replication;
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75591 MW; B53F76D9F9FBD613 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (or send an email to license@isb-sib.ch)
    (strain Kresse)
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                                                                                               SEQUENCE FROM N.A.
MEDLINE=96183900; Pubmed=8642680;
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       Porcine parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   662 AA;
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                                             NCBI_TaxID=73487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-binding
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VNCS_FPV19
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G -> R (IN REF. 2).

K -> R (IN REF. 2).

C -> V (IN REF. 2).

TALTQHARFSNTDT -> NLHLTPTPPDSAIRTP (IN
                                                                                                                                      Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus
NCBI_TaxID=10797;
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Ranz A.I., Manclus J., Diaz-Aroca E., Casal J.I.;
"Porcine parvovirus: DNA sequence and genome organization.";
J. Gen. Virol. 70:2541-2553(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 367-660 FROM N.A. MEDLINE-90085785; PubMed-2596019; Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.; Vasudevachae sequence analysis of the capsid genes and the riterminal palindrome of porcine parvovirus, strain NADL-2."; Virology 173:368-377(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 99; DB 1; Length 660;
Pred. No. 7.2e-09;
0; Mismatches 1; Indels
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COBIDF2226A2EF0A CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
01-NOV-1990 (Rel. 16, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NSI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              662 AA.
                                                                                                                   Porcine parvovirus (strain NADL-2) (PPV)
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95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 parvovirus, strain NADL-2.
Virology 178:611-616(1990)
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Best Local Similarity 95.0°
Marches 19, Conservative
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86
274
376
634
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                                                                                                                                                                                                              SEQUENCE FROM N.A.
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CONFLICT
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ID VNCS PAVI
AC P52502;
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-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=193770;
MEDLINE=91073139; PubWed=2174965;
Martyn J.C., Davidson B.E., Studdert M.J.;
Martyn J.C., Davidson B.E., Studdert M.J.;
"Nuclocided sequence of felline panleukopenia virus: comparison with
canine parvovirus identifies host-specific differences.";
J. Gen. Virol. 71:2747-2753 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mapping specific functions in the capsid structure of canine parvovirus and feline panleukopenia virus using infectious plasmid
                                                                                                                                                                                                                                                                                                                                            ssDNA viruses; Parvoviridae; Parvovirus.
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96.1%; Score 99; DB 1; Length 662; 95.0%; Pred. No. 7.2e-09; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                      01-MAR-1992 (Rel. 21, Created)
1-MAR-1992 (Rel. 21, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
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à 셤 GETTTE

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PAVCN
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P12929;
                                                                                                                     RESULT 6
VNCS_PAVCN
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOLO H., Shinagawa M.;
GOLO H., Shinagawa M.;
"Construction and nucleotide sequence analysis of an infectious DNA clone of the autonomous parvovirus, mink enteritis virus.";
J. Gen. Virol. 72:867-875(1991).
-:- FUNCTION: Seems necessary for viral DNA replication.
-:- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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Kariatsumari T., Horiuchi M., Hama E., Yaguchi K., Ishigurio N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
                                                                                                                                                                              SMART; SM00382; AAA; 1.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                            Score 99; DB 1; Length 668; Pred. No. 7.3e-09;
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                                                                                                                                                                                                                                                                                                                       1; Indels
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76736 MW; DBD5F9E92113685C CRC64;
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I -> V (IN REF. 2).
I -> N (IN REF. 2).
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Mink enteritis virus (strain Abashiri) (MEV)
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                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                         EMBL, M38246; AAC37927.1; -.
PIR, A36608; UTPVFP.
INTERPRO; IPR003593; AAA_ATPase.
INTERPRO; IPR001257; Parvo_NS1.
PF01057; Parvo_NS1; I.
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InterPro; IPR001257; Parvo NSI.
PFam; PF01057; Parvo_NSI; I.
SMART; SM00382; AAA, 1.
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95.0%;
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                                                                                              EMBL; X55115; CAA38910.1; -.
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Reed A.P., Jones B.V., Miller T.J.;
"Nucleotide sequence and genome organization of canine parvovirus.";
J. Virol. 62:266-276(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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  Length 668;
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Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
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DE2CCEA69D2A63A6 CRC64;
                                                                                                                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
1-OCT-1989 (Rel. 12, Last sequence update)
15-DBC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
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01-JUN-1994 (Rel. 29, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1)
96.1%; Score 99; DB 1; I 95.0%; Pred. No. 7.3e-09; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                   668 AA.
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EMBL; M36245; AAB02798.1; -.
EIR; A29962; UYPVCP.
InterPro; IPR0013593; AAA_ATPase.
InterPro; IPR001257; Parvo_NS1.
Ffam; PF01057; Parvo_NS1.
SNART; SM00382; AAA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canine parvovirus (strain N) (CPV)
                                                                                                                                 462 GQTIRIDQKGKGSKQIEPTP 481
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                                                                                                    1 GOAIRIDQKGKGSKQIEPTP 20
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Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                   STANDARD;
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P36311;
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ATP-binding.
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                                                                                                                                                         NP BIND
CONFLICT
SEQUENCE
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VNCS_MUMIV
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                SSSSS RABBANTES
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                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute: There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                            -1- FUNCTION: Seems necessary for viral DNA replication.
-1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=85242059; Dubwed=3855242; Sahli R., McMaster G.K., Hirt B.; "Shli R., McMaster G.K., Hirt B.; "DNA sequence comparison between two tissue-specific variants of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=86115415; PubMed=3502703;
Astell C.R., Gardiner E.M., Tattersall P.;
Astell C.R., Gardiner Lymphotropic variant of minute virus of mice,
"DNA sequence of the lymphotropic variant of minute virus of mice,
MVM(1), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine minute virus (strain MVMi) (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10795;
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=35339;
                                                                    MEDIINE-93297126; PubMed-8517025; Diffoot N., Chen K.C., Bates R.C., Lederma M.; The complete nucleotide sequence of parvovirus LuIII and localization of a unique sequence possibly responsible for its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.1%; Score 99; DB 1; Length 668; 95.0%; Pred. No. 7.3e-09; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P07370; P10837; Created) (1-APR-1988 (Rel. 07, Created) (1-JUL-1988 (Rel. 17, Last sequence update) (15-DEC-1998 (Rel. 37, Last annotation update) (NCVPI). Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVPI).
                                                                                                                                                                                                                                                                                                                                                                               Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autonomous parvovirus, minute virus of mice.";
Nucleic Acids Res. 13:3617-3633(1985).
-!- FUNCTION: Seems necessary for viral DNA replication.
                                                                                                                                                                                                                                                                                                                                                                                                          TP (POTENTIAL).
CAE69049F8F86B53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             672 AA
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                                                                                                                                                                                                                                                                                                                    EMBL; M81888; -; NOT ANNOTATED CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              461 GOTIRIDOKGKGSKOIEPTP 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                       668 AA; 75846 MW;
                                                                                                                                 encapsidation pattern.";
Virology 192:339-345(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             totype strain.";
Virol. 57:656-669(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 95.0
nes 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           406
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A03696; UYPVIM.
TRANSFAC; T02375; -.
ITLEPIPO; IPRO01257; Parvo_NS1.
Pfam; PPO1057; Parvo NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
                                                                                                        EMBL; X02481; -; NOT ANNOTATED CDS.

EMBL; M12032; AAA69567.1; -.

InterPro; IPR001257; Parvo NS1.

Pfam; PF011057; Parvo NS1; I.

Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                     Length 672;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                        7399 406 ATP (POTENTIAL).
597 597 I -> L (IN REF. 2).
672 AA; 76140 MW; 25F025FE328B4DF0 CRC64;
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76248 MW; 50298F27662E3CID CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   Score 99; DB 1; I
Pred. No. 7.3e-09;
                                                                                                                                                                                                                                                       ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                               96.1%; Scor.
95.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J02275; AAA67109.1; -.
EMBL; V01115; CAA24309.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-83143341; PubMed=6298737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              461 GOTIRIDOKGKGSKOIEPTP 480
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Best Local Similarity 95.0
Matches 19; Conservative
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Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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SYNY3
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SEQUENCE
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P73440;
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YES9 SYNY3
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MEDLINE=83164299; PubMed=6300419;
Srivastava A., Lusby E.W., Berns K.I.;
"Nucleotide sequence and organization of the adeno-associated virus 2
                                                                                                                                                                                                                                                                                                                                                                                      J. Virol. 45:173-184(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
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                                                                                                                                                                                                          Viruses, seDNA viruses, Parvoviridae, Parvovirinae, Parvovirus.
NCBI_TaxID=10799;
                                                                                                                                                                                                                                                                                                                                         "Parvovirus genome: nucleotide sequence of H-1 and mapping of genes by hybrid-arrested translation."; J. Virol. 45:173-184(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.1%; Score 99; DB 1; Length 672; 95.0%; Pred. No. 7.3e-09;
                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
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21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA replication protein (Noncapsid protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Virol. 45:555-564(1983).
-!- FUNCTION: ESSENTIAL FOR DNA REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     536 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=83112183; PubMed=6823009;
Rhode S.L. III, Paradiso P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461 GOTIRIDOKGKGSKOIEPTP 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                          STANDARD;
                                                                                                                                                                                           Hamster parvovirus H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A03695; UYPVV1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     672 AA;
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NCBI_TaxID=10804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding.
                                        VNCS PAVHH
P03133;
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VNCA AAV2
ID VNCA AAV2
AC P03132;
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                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
non-profit institutions as long as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97061201; PubWed=8905231; Kanaka A., Asamizu E., Nakamura Y., Kanoko T., Sato S., Kocani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosamu, Sugiura M., Sasamoto S., Kimura T., Miyajima N., Maruno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yanada M., Tabata S., Yanada M., Tabata S., Shimpo S., Takeuchi C., Mada T., Watanabe A., Saguence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 3:109-136(1996).
-!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alcohol + phosphate.
-!- COFACTOR: Magnesium (By similarity).
-!- SIMILARITY: Belongs to the surE acid phosphatase family.
                                                                                                                                                                                                                                                                                                                                                                                  Score 67; DB 1; Length 536;
Pred. No. 0.0016;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).
; 7C1ECDD4E07703C8 CRC64;
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METAL 8 MAGNESIUM (BY SIMILARITY)
METAL 9 9 MAGNESIUM (BY SIMILARITY)
METAL 37 37 MAGNESIUM (BY SIMILARITY)
METAL 88 88 MAGNESIUM (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-ROV-1997 (Rel. 31, Last annotation update)
Putative acid phosphatase sll1459 (EC 3.1.3.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 GSKVRVDQKCKSSAQIDPTP 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GOAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
24907 MW; 4
                                                                                                                                                                                                       InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; 1.
                                                                                                                                                                                                                                                                                                                                 536 AA; 60754 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR, 577377; S77377.
HAMAP, MF 00060; atypical, 1.
InterPro, IPR002828; SurE.
                                                                                                                                                                                                                                                                  DNA replication; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                         65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01975; SurE; 1.
ProDom; PD005378; SurE; 1.
TIGRFAMS; TIGR00087; surE; 1.
                                                                                                                                            EMBL; J01901; AAA42372.1; -. PIR; A03694; UYADIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D90906; BAA17480.1; -.
                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 60.09
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
120 1
225 AA;
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CORGL
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                       ò
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          denome Res. /3:1572-1579(2003).
-!- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-phosphoribosyl)amino)methylideneamino] imidazole-4-carboxamide :phosphoribosylomino)methylideneamino] imidazole-4-carboxamide | (5-phosphor-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-carboxamide | -!- PATHWAY: Histidine biosynthesis; fourth step. -!- SPATHWAY: Histidine biosynthesis; fourth step. -!- SPATHARITY: Belongs to the hisA / hisF family.
                                                                                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1- (S-phosphoribosyl) -5-[(S-phosphoribosylamino)methylideneamino]
imidazole-4-carboxamide isomerase (EC 5.3.1.16)
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E., Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K., Gojobori T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.7%; Score 46; DB 1; Length 246; 45.0%; Pred. No. 2.7;
                       DB 1; Length 225;
                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Arver-
HAMAP; MF 01014; -; 1.

HAMAP; MF 01014; -; 1.

InterPro; IPR006063; His4.

InterPro; IPR006062; His biosynth.

Pfam; PF0977; His biosynth; 1.

TIGREAMS; TIGR00067; TIGR00007; 1.

Isomerase; Histidine biosynthesis; Complete proteome.

246 AA; 26624 MW; EF62454178C09B50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036;
                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                       Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 GOAVRLDOGEAGTEKSYGTP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                          |||| ::|:||
QAIAVEQRGKNRYAVDGTP 65
                                                                                                             2 QAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP005220; BAC18806.1; -.
                44.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.0%;
Query Match
Best Local Similarity 42.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
tes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HISA OR CE1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 efficiens.";
                                                                                                                                                                                                                                                                           HIS4 COREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   somerase
                                                                                                                                                           47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                             RESULT 13
HIS4_CORE F
ID HIS4_CORE F
ID T 10-OCT
DT 10-OCT
DT 10-OCT
DE imids-
DE imids-
DE imids-
DE imids-
DE CORP
DE CORP
OC Bacter
OC CORP
RA NISH
RA NISH
RA NISH
RA SUGHM
RA NISH
RA GOJOB
RT "COMPE
RT 
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Matches
                                                                                                                8
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RESULT 14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.", Submitted (MAY-2002) to the EMBL/GenBank/DDBJ datebases.
-!- CATALYTIC ACTIVITY: 1 - (5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosylamino)] methylideneamino] imidazole-4-carboxamide = 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                           28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino)
imidazole-4-carboxamide isomerase (EC 5.3.1.16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ī)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                (Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide
                                                                                                                                                                                                                                                                         Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G -> S (IN REF. 1).
ERA -> DTQ (IN REF. 1).
A -> L (IN REF. 1).
RYGEKLAUD -> AMARELLS (IN REF. 1).
R -> C (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.7%; Score 46; DB 1; Length 246; 45.0%; Pred. No. 2.7; ive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 13059 / AS019;
Jung S.I., Han M.S., Park Y.J., Lee M.-S.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphoribosyl)imidazole-4-carboxamide.
--- PATHWAY: Histidine biosynthesis; fourth step.
--- SUBCELIULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Belongs to the hish / hisF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6A35CF9153C32B1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HANNEY ME 1014; -; 1.
InterPro; IPR003009; FMN_enzyme.
InterPro; IPR006062; His4.
InterPro; IPR006062; His4.
InterPro; IPR00707; His biosynth.
IGRPAMs; TIGR00007; TIGR00007; 1.
ISOMerase; Histidine biosynthesis; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IN REF.
246 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIVA -> TYLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF051846; AAC05575.1; -. EMBL; AP005280; BAB99489.1; -. PIR; JE0213; JE0213.
                                                       (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26609 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 ĠġÁVŘLĎĢGEAĞTEKSYGŤP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
92
105
127
157
198
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119
157
195
246 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        HISA OR CGL2096.
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TP6A AERPE
ID TP6A AERPE
AC Q9YE67;
                                                                                                                                                                                                                                isomerase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
                                                                                                                                                                                                                                                                      Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H., "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: Binds 1 magnesium ion per subunit (By similarity).
-!- SUBUNIT: Heterotetramer of two subunits A and two subunits B (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lsomerase; Topoisomerase; DNA-binding; Metal-binding; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Relaxes both positive and negative superturns and exhibits a strong decatenase activity (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.7%; Score 46; DB 1; Length 385; 45.0%; Pred. No. 4.3; tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 103 DNA CLEAVAGE (BY SIMILARITY)
204 204 MAGNESIUM (BY SIMILARITY).
256 256 MAGNESIUM (BY SIMILARITY).
385 AA; 45012 MW; 19CBCB88728F3D37 CRC64;
                                                                                                                             Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Desulfurococcaceae, Aeropyrum.
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Type II DNA topoisomerase VI subunit A (EC 5.99.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIMILARITY: Selongs to the TOP6A family.
                                                                                                                                                                                                                                                                                                                                                                                                                crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                         MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, Q57815, 1D3Y.
HAMAP; MF 00132; -; 1.
InterPro; IPR004085; DNA top6A.
InterPro; IPR002815; DNA topII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP000060; BAA79679.1; -. PIR; G72659; G72659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS, PRO1550; TOPGAFAMILY.
PRINTS; PRO1552; TPISMRASEGA.
ProDom; PD008669; DNA_topII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 45.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF04406; TP6A N; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID=56636;
                                                                                                                     Aeropyrum pernix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Search completed: May 28, 2004, 12:57:44 Job time : 7.75 secs

1 GQAIRIDQKGKGSKQIEPTP 20
| | : : | |: |||||
6 GDVIDLSKLGHGAYAIEPTP 187

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murine minu murine minu bovine parv

minute minute goose parvo muscovy duc

barbarie du goose parvo goose parvo adeno-assoc

adeno-assoc

adeno-assoc adeno-assoc adeno-assoc adeno-assoc adeno-assoc adeno-assoc

pig-tailed simian parv rhesus maca

chipmunk pa adeno-assoc hamster par

adeno-assoc adeno-assoc avian adeno

adeno-assoc

Sequence:

Title:

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Searched:

Database

Result No.

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STRAIN=Yale;
MEDLINE=2110299; PubMed=11172095;
Ball-Goodxich L.J., Johnson E., Jacoby R.;
Ball-Goodxich L.J., Johnson E., Jacoby R.;

Bill-Goodxich L.J., Johnson E., Jacoby R.;

Divergent replication kinetics of two phenotypically different parvoviruses of rate.";

J. Gen. Virol. 82:53-546(2001).

EMBL, AF317513; AAK27438.1; -.

InterProj. IPR001257; Parvo. NS1.

Pfam, PF01057; Parvo. NS1.

Pfam, PF01057; Parvo. NS1.
                                                                                                                                                                                                                                                                                                                  Autonomous rat parvovirus RV-Y.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=155025;
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96.1%; Score 99; DB 12; Length 397;
Best Local Similarity 95.0%; Pred. No. 5.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels
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Q67465
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SEQUENCE FROM N.A.
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                                                  May 28, 2004, 12:52:08 ; Search time 32 Seconds
       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                               1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
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sp_bacteria:*
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sp_human:*
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Horiuchi M.; "Evolutionary pattern of feline panleukopenia virus differs from that
                   Nonstructural protein 1.
Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB000069; BAA19030.1; -.
EMBL; AB0000605; BAA19034.1; -.
GO; GO:0019012; C:vIrion; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
                                                                                                                                                                                                           of canine parvorirus.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AB000057; BAA1901B.1;
GO; GO:0000166; F:nucleotide binding; IEA.
InterPro; IPR001593; AAA_ATPase.
InterPro; IPR001257; Parvo_NSI.
EFfan; PR01057; Parvo_NSI.
SMART; SM00382; AAA; 1.
SEQUENCE 668 AA; 76741 MW; 2413E450EC9161BD CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 9.8e-08;
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InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; 1.
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Nonstructural protein.
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                                                                                                                                                                                                                                                                                                   "Rat parvovirus type 1: the prototype for a new rodent parvovirus
                                                                                                     Kilham rat virus.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=12441;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=10786;
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Ball-Goodrich L.J., Leland S.E., Johnson E.A., Paturzo F.X.,
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Pred. No. 9.7e-08;
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InterPro; IPR003593; AAA ATPase.
InterPro; IPR0157; Parvo NS1.
Pfam; PF01057; Parvo NS1; 1.
SWART; SM00382; AAA; 1.
SEQUENCE 668 AA; 76755 MW; 37ABDFD347017F52 CRC64;
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Last annotation update)
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                                                             Nonstructural protein (Fragment)
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J. Virol. 72:3289-3299(1998).
EMBL, AF036711; AAC40695.1; -.
InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; I.
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RESULT 3 P89516

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Horiuchi M., "Evolutionary pattern of feline panleukopeina virus differs from that of canine parvovirus.";
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Horiuchi M.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AB000060; BAA19021.1;
                                                                                                                                                      Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                      EMBL, AB000051, BAA19012.1; -. GO; GO:000166; F:nucleotide binding; IEA.
InterPro; IPR003533; AAA ATPase.
InterPro; IPR01257; Parvo NS1.
Pfam; PF01057; Parvo NS1; 1.
SWART; SM00382; AAA; 1.
SEQUENCE 668 AA; 76770 MW; 1B9EFE7136308720 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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EMBL; AB000049; BAA19010.1; -.
EMBL; AB000058; BAA19019.1; -.
GO; GO:0019012; C:virion; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
InterPro; IPR001257; Parvo_NS1.
Fam; PF01057; Parvo_NS1.
SWART; SM00382; AAA; 1.
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Feline panleukopenia virus (FPV)
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Nonstructural protein
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  NCBI_TaxID=10786;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10786;
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                                                                                                                                                Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB000067; BAA19028.1; -.
EMBL; AB000065; BAA19026.1; -.
GO; GO:0019012; C:virion; IEA.
GO; GO:0010166; F:nucleotide binding; IEA.
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SMART; SM00382; AAA; I.
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, AB000015; BAA19011.1; -...
GO, GO:0000166; F:nucleotide binding; IEA.
InterPro; IPR001593; AAA ATPase.
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1.
SMART; SM001382; AAA; 1.
SEQUENCE 668 AA; 76743 MW; 84A210104D9D5788 CRC64;
                                                                                                                                                                                                                                                                                                                                                      Nonstructural protein.
SEQUENCE 668 AA; 76755 MW; 008CED50178833EF CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                      SEQUENCE FROM N.A.
                                      NCBI.TaxID=10786;
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                                                                                                                                    Horiuchi M.;
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RESULT 8 P89512 AC P8955 DT 01-M DT 01-M DT 01-O DE NOUS

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"Rat parvovirus type 1: the prototype for a new rodent parvovirus
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=172385;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=12441;
                                                       Rat parvovirus 1a.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=74581;
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MEDLINE-22120170; PubMed=12124471;
WAN C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
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J. Gen. Virol. 83;2075-2083(2002).
EMBL; AF332882; AAM93275.1; -.
InterPro; IPR011257; Parvo NS1.
Pfam; PF01057; Parvo NS1; Ī.
SEQUENCE 672 AA; 76059 MW; 63D8B9EBF99E07B3 CRC64;
                                                                                                                                                                                                                                                                                     EMBL, AF036710; AAC40693.1; -.
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; T.
SEQUENCE 671 AA; 75752 MW; 9BCB39A39298D4DE CRC64;
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    01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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95.0%; Pred. No. 9.8e-08;
iive 0; Mismatches 1
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MEDLINE=98184569; PubMed=9525656;
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J. Virol. 72:3289-3299(1998).
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Best Local Similarity 95.09
Watches 19; Conservative
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                         Nonstructural protein.
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Q8JV18
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"Evolutionary pattern of feline panleukopenia virus differs from that
"Of canine parvovirus.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                         Horiuchi M., Goto H., Ishiguro N., Shinagawa M.; "Mapping of determinants of the host range for canine cells in the genome of canine parvovirus using canine parvovirus/mink enteritis virus chimeric viruses."; J. Gen. Virol. 75:1319-1328(1994).

EMBL; D26079; BAA05072.1;
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                                                             STEAIN=Y1; Horiuchi M.; Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
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GO; GO: 000166; F:nucleotide binding; IEA.
INTERPRO; IPR001559; AAA ATPASE.
INTERPRO; IPR001257; PATVO NSI.
Pfam; PR01057; PATVO NSI.
SEQUENCE 668 AA; 1.
SEQUENCE 668 AA; 76724 MW; C038269E428612B3 CRC64;
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SEQUENCE 668 AA; 76755 MW; 1D72C5E85DBA430F CRC64;
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Last sequence update)
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MEDLINE=94267414; PubMed=8207398;
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InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; I.
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01-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
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P89514;
01-MAY-1997 (TrEMBLrel. 03,
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Feline panleukopenia virus
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Best Local Similarity 95.0
Matches 19; Conservative
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NCBI_TaxID=10788;
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MEDLINE=94365951; PubMed=8083985;

Ball-Goodrich L.J., Johnson B.;
"Molecular characterization of a newly recognized mouse parvovirus.";
J. Virol. 68:6476-6486(1994).

SEQUENCE FROM N.A.

Ball-Goodrich L.J.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.

EMBL, Ju2469; AAA644055.1; -.
InterPro; IPR001257; Parvo NS1.
InterPro; IPR001257; Parvo NS1.
SEQUENCE 672 AA; 76112 MW; 31C6365276727363 CRC64;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=35340;
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96.1%; Score 99; DB 12; Length 672;
Best Local Similarity 95.0%; Pred. No. 9.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 95.0%; Pred. No. 9.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                     Brown D.W., Like A.A.;
Brown D.W., Like A.A.;
"Sequence of a Diabetogenic Parvovirus of Rats.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; UJ9033; AAB38326.1; -.
InterPro; IPGD157; Parvo NS1.
Pfam; PP010F7; Parvo NS1.
SEQUENCE 672 AA; 76056 MW; 0299B36871A0A10A CRC64;
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Last annotation update)
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SEQUENCE FROM N.A.
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Search completed: May 28, 2004, 13:00:05 Job time : 33 secs

461 GQTIRIDQKGKGSKQIEPTP 480

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NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 11, Appl
Sequence 1111, Ap
Sequence 17887, A
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Sequence 4848, Ap
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Sequence 19264, A
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Sequence 5503, Ap
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Sequence 22466,
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                                                                                   May 28, 2004, 12:53:44; Search time 13.5 Seconds (without alignments) 76.483 Million cell updates/sec
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Sequence 5,
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-532-594B-9

US-09-532-594B-10

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US-09-001-273-8

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US-09-01-273-2

US-09-347-798-12

US-09-347-59-12

US-08-456-45-5

US-08-457-66A-5

US-08-252-91A-19269

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                                                                                                                                                                                                                                                   389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
                                                                                                                                                                        GOAIRIDQKGKGSKQIEPTP 20
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Gapop 10.0 , Gapext 0.5
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Sequence 30336, A Sequence 5229, A Sequence 5229, A Sequence 4323, Ap Sequence 30326, A Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2034, A Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 22702, A Sequence 30109, A			e; No. 6468524e =	gth 312; Indels 0; Gaps 0;		
US-09-252-991A-30336 US-09-255-991A-32992 US-09-107-532A-529 US-09-252-991A-30326 US-09-252-991A-30326 US-08-695-355-1 US-08-695-355-1 US-08-695-35-1 US-09-063-869-1 US-09-063-869-1 US-09-252-991A-28234 US-09-252-991A-2014 US-08-477-666-1 US-08-477-666-1 US-08-477-666-1 US-09-252-991A-2702 US-09-252-991A-2702 US-09-315-793-52	ALIGNMENTS	9532594B.  1y  CTOR AND USES THEREOF US/09/532,594B 03-22 ws Version 4.0	h: 312 PRT 18M: Artificial Sequence RE: INFORMATION: Description of Artificial Sequence; INFORMATION: synthetic construct KRY: misc feature INFORMATION: AAV4 Rep protein 40	Score 67; DB 4; Len Pred. No. 0.004; ; Mismatches 5; 20	 	1532594B TOR AND USES THEREOF US/09/532,594B
782 4 807 4 907 4 909 4 1044 4 177 4		nn US/09532594B obn A. ian Beverly AV4 VECTOR AND .0252U 2000-03-22 2200-03-22 Windows Versic	ial Sequence : Description of A: : synthetic construature : AAV4 Rep protein	65.0%; 60.0%; ative	: KSSAQIDP	n US/0955 Ohn A. ian ian Beverly AV4 VECTU UMBER: UE
88887777777777777777777777777777777777		RESULT I US-09-532-594B-8 Sequence 8, Application US/09532594B Patent No. 646854 GENERAL INFORMATION: APPLICANT: Chorini, John A. APPLICANT: Kotin, Robert M. APPLICANT: Safer, Brian APPLICANT: Baridson, Beverly ITILE OF INVENTION: AAV4 VECTOR AND TILLE OF INVENTION: AAV4 VECTOR AND CURRENT APPLICANION NUMBER: US/09/5 CURRENT FILING DATE: 2000-03-22 NUMBER OF SEQ ID NOS: 22 SECTION OF SEQ ID NOS: 22 SECTION OF SEQ ID NOS: 22	LEWGTH: 312 TYPE: PRT OKGANISM: Artificial FEATURE: OTHER INFORMATION: BY OTHER INFORMATION: GY OTHER INFORMATION: AA 9-532-594B-8	65.0%; imilarity 60.0%; ; Conservative 3 GQAIRIDQKGKGSKQIEPTP	: :        :    GSKVRVDQKCKSSAQIDPTP	Scource 2 S-09-532-594B-9 Sequence 9, Application US/0953259. Sequence 9, Application US/0953259. Batent No. 6466524 GENERAL INFORMATION: APPLICANT: Chorini, John A. APPLICANT: Safer, Brian APPLICANT: Safer, Brian APPLICANT: Bavidson, Beverly TITLE OF INVENTION: AAV4 VECTOR AF FILE REFRENCE: 14014.0252U2 CURRENT FILING DATE: 2000-03-22 NUMBER OF SEQ ID NOS: 22
м 4444000000000000000000000000000000000		RESULT 1 US-09-53-594B-8 Sequence 8, Applica' Patent No. 6468524 GENERAL INFORMATION APPLICANT: Chorin, APPLICANT: Rotin, APPLICANT: Bafer, CURRENT ELING DATI, NUMBER OF SEQ ID NO. SOFTWARR: FaetSEQ. SOFTWARR: FaetSEQ. SOFTWARR: FaetSEQ. SOFTWARR: FaetSEQ.	LENGIH: 312 TYPE: PRT ORGANISM: Art FEATURE: OTHER INFORMA OTHER INFORMA OTHER INFORMA OTHER INFORMA 9-532-594B-8	ttch 3al 8 12	172 G	RESULT 2 US-09-532-594B-9 Sequence 9, Applicat Patent No. 646B524 GENERAL INFORMATION: APPLICANT: Kotin, APPLICANT: Safer, APPLICANT: Safer, APPLICANT: Davidso TITLE OF INVENTION: FILE REFERENCE: 140 CURRENT PAPLICATION: CURRENT PAPLICATION: CURRENT PAPLICATION: NUMBER OF SEQ ID NO
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NAMMS/KEX: misc feature
CTHER INFORMATION: AAV4 Rep protein 68
US-09-532-594B-10
                                                                                                          CTHER INFORMATION: Description of Artificial Sequence; No. 6468524e; OTHER INFORMATION: synthetic construct
NAME/KEY: misc_feature
CTHER INFORMATION: AAV4 Rep protein 52
US-09-532-5948-9
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Pred. No. 0.0052;
3; Mismatches 5; Indels
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APPLICANT: Kotin, Robert M.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
FILE REPERENCE: 14014.0252U2
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 623
TYPE: PRT
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APPLICANT: Chorini, John A.
APPLICANT: Safer, Brian
APPLICANT: Safer, Brian
TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
FILE REFERENCE: 14014.0252U2
CURRENT APPLICATTON NUMBER: US/09/532,594B
CURRENT FILING DATE: 200-03-22
NUMBER OF SEC ID NOS: 22
SOFTWARE: FSELSEQ for Windows Version 4.0
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; Patent No. 6468524
; GENERAL INFORMATION:
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                                              TYPE: PRT .
ORGANISM: Artificial Sequence
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Best Local Similarity 60.0%
Matches 12; Conservative
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LENGTH: 536
SEQ ID NO 9
LENGTH: 399
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US-09-329-352-8111
US-09-328-352-8111

Sequence 8111, Application US/09328352

Patent No. 656298

GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 8111

LIENGTH: 730
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OTHER INFORMATION: Description of Artificial Sequence; No. 6468524e; OTHER INFORMATION: synthetic construct
NAMB/KEY: misc_feature
1 OTHER INFORMATION: AAV4 Rep protein (full length)
US-09-532-594B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence; No. 6468524e;
OTHER INFORMATION: synthetic construct
NAME/KEY: misc_feature

NAME/KEY: misc_feature
US-09-532-5948-11
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                                                                                                                                              Score 67; DB 4; Length 623;
Pred. No. 0.0085;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 67; DB 4; Length 623; Pred. No. 0.0085; 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
ITILE OF INVENTION: AAV4 VECTOR AND USES THEREOF
FILE REFERENCE: 14014.0252U2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 43.7%; Score 45; DB 4; Best Local Similarity 50.0%; Pred. No. 38; Matches 7; Conservative 5; Mismatches ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 623
                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-09-532-594B-11
Sequence 11, Application US/09532594B
Patent No. 6468524
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              396 GSKVRVDQKCKSSAQIDPTP 415
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                                                                                                                                                                                                                                               1 GOAIRIDOKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Acinetobacter baumannii US-09-328-352-8111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                 Query Match
Best Local Similarity 60.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.0%;
Best Local Similarity 60.0%;
Matches 12; Conservative
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Sequence 38, Application US/10162012
Sequence 38, Application US/10162012
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Gl, Weil
APPLICANT: Gl, Weil
APPLICANT: Gl, Weil
APPLICANT: OG WINDER: US/10/162,012
CURRENT APPLICATION NUMBER: US/10/162,012
CURRENT APPLICATION NUMBER: US/002-06-06
PRIOR PILING DATE: 2000-06-06
PRIOR PLING DATE: 2001-06-06
PRIOR PLING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/209,257
PRIOR PLING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/209,257
PRIOR PLING DATE: 2001-06-05
PRIOR PLING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/209,238
PRIOR PLING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/209,238
PRIOR PLING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/209,238
PRIOR PLING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/209,238
PRIOR PLING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/207,068
PRIOR PLING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/227,068
PRIOR PLING DATE: 2001-06-05
PLING DATE: 2001-06-05
PLING DATE: 2001-06-05
PLING DATE: 2001-06-05
PLING DATE: 2001-06-05
PLING DATE: 2001-06-05
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                                                                                                                                 40.8%; Score 42; DB 3; Length 1437;
46.2%; Pred. No. 2.5e+02;
ive 6; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: US 60/290,288
PRIOR PILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US (not assigned)
PRIOR PILING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/USO1/25475
PRIOR FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: US 60/226,770
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 09/934,421
PRIOR FILING DATE: 2010-08-21
PRIOR PLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/279,281
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 10/109,029
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: PCT/US02/09728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 38, Application US/10162012
                                                                                                                                                                                                                                                                                                                828 GQLVQLEEKGQGS 840
                                                                                                                                                                                                                                                                      1 GQAIRIDQKGKGS 13
                                                                                                                                                                 Best Local Similarity 46.2
Matches 6; Conservative
                               , MOLECULE TYPE: protein US-09-061-400-2
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-10-162-012-38
                                                                                                                                        Query Match
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                                                                                                                                                                                                                                          GENGRAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

ATTLE OF INVENTION: APRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILLE REFERENCE: 10196-102-18

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 476
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Sequence 2, Application US/09061400

Fatent No. 6077936

GENERAL INFORMATION:

APPLICANT: SHYJAN, Andrew

TITLE OF INVENTION: POLYPEPTIDE

TITLE OF INVENTION: POLYPEPTIDE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STREET: 28 State Street

CITY: Boston

STREET: AMSSACHUSELTS

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: BRACHIN RELAGESHED:

SOFTWARE: PRECHIN DATA:

RELICATION NUMBER: US/09/061,400

FILING DATE: 16-APRIL-1998

FILING DATE: 16-APRIL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 4; Length 476;
Pred. No. 74;
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ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REGISTRATION COCKET NUMBER: MNI-056CP
TELECOMMUNICATION:
TELECOMMUNICATION:
(617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match .40.8%;
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                             :|:||| :| :||
608 LDKKGKKAKTVDPT 621
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1437 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1437 amino acids
                                      6 IDQKGKGSKQIEPT 19
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.8%;
                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1453 amino acids
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844 GQLVQLEEKGQGS 856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-134-001C-4848
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 DB 4; Length 1437;
                                                                                                                                                                                                Sequence 2, Application US/09001273
Patent No. 5994130
GENERAL INFORMATION:
APPLICANT: SHYADA, Andrew
TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High &t.
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1453;
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Patent No. 6162616.
GENERAL INFORMATION:
APPLICANT: SHYJAN, Andrew
TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 8
NORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE: ADDRESSE:
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001,273
                 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5e+02;
40.8%; Score 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: FENTON, Gillian M
REGISTRATION NUMBER: 36,508
REPERENCE/DOCKET NUMBER: MIL-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.2%;
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828 GQLVQLEEKGQGS 840
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844 GQLVQLEEKGQGS 856
                                                                         1 GQAIRIDQKGKGS 13
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                                  Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Massachusetts
: USA
                 Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: Massach
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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US-08-843-459A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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 Query Match
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Sequence 4848, Application US/09134001C

Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DEPERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4848
LENGTH: 404
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40.3%; Score 41.5; DB 4; Length 404;
Best Local Similarity 55.0%; Pred. No. 75;
Matches 11; Conservative 2; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1453;
                                                                                                                                                                    NAME: Hanley, Elizabeth A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-056 (formerly MLL-001)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)722-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,459A FILING DATE: 16-APR-1997 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 3; 1
Pred. No. 2.5e+02;
6; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09347798
Patent No. 6242256
GENERAL INPORMATION:
APPLICANT: Cahoon, Edgar B.
APPLICANT: Cahoon, Rebeca E.
APPLICANT: Hitz, William D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GOAIRIDOKG-KGSKOIEPT 19
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                                                                                                              Query Match 39.8%; Score 41; DB 1; Length 363; Best Local Similarity 35.0%; Pred. No. 80; Matches 7; Conservative 4; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 01-UN-1995
CLASSIFICATION: 435
PAPPLICATION DATA:
APPLICATION NUMBER: 08/457,205
FILING DATE: 01-UN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Un-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Gaigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
                                                                                                                                                                                                                                99 GQCVHIPGHNQAVRQLEPVP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaffney, Thomas Deane
                                                                                                                                                                                                                                                                                                                                                                                                                T: Schupp, Thomas
T: Ligon, James M.
T: Beck, James Doseph
T: Hill, Daight Steven
T: Ryals, John Andrew
                                                                                                                                                                                                   1 GOAIRIDOKGKGSKOIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GOAIRIDOKGKGSKOIEPTP 20
                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08456837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lam, Stephen Ting
Hammer, Phillip E.
Uknes, Scott Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-456-837-5
                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-258-2618-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO
      amino acid
XGY: linear
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                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5643774
GENERAL INFORMATION:
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Pred. No. 79;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: FLOURY GENERAL COMPUTER: FLOURY GENERAL BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/258,261B FILING DATE: 08-JUN-1994 CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/457,205 FILING DATE: 01-JUN-1995 ATTORNEY/AGENT INPOMENTION: NAME: Elmer, James Scott REGISTRATION NUMBER: 36,129
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Ornithine Biosynthesis Enzymes
FILE REFERENCE: BB-1174-B
CURRENT APPLICATION NUMBER: US/09/347,798
CURRENT FILING DATE: 1999-07-02
BARLIER APLICATION NUMBER: 60/093,209
BARLIER PILING DATE: July 17, 1998
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Microsoft Office 97
SEQ ID NO 1:
LENGTH: 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Hammer, Phillip E.
APPLICANT: Hammer, Phillip E.
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF SEQUENCES: 2
CORRESPONDENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: Ciba-Geigy Corporation
: 7 Skyline Drive
Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08258261B
Patent No. 5639949
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 GVAİRİGGMAKGSGMİHP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GQAIRIDQKGKGSKQIEP 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 39.8%;
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Zea mays
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; LOCATION: (288)
US-09-347-798-12
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STREET: 7
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US-08-258-261B-5
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Thu Jun 3 10:28:25 2004

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99 GQCVHIPGHNQAVRQLEPVP 118

Search completed: May 28, 2004, 13:02:04 Job time : 13.5 secs

Appl Appl Appl Appl Appl

Sequence 29,

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Minimum DB Maximum DB

Database

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Sequence 33, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 27, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 3, Appli
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Sequence 3, Appli
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Sequence 3, Appli
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Sequence 27, Sequence 27,
Sequence 27,
Sequence 27,
Sequence 27,
Sequence 27,
Sequence 27,
                                               Sequence 35
Sequence 29
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Publication No. US20030129203A1

GENERAL INFORMATION:
APPLICANT: Vega, Manuel
APPLICANT: Plaux, Marjorie
TITLE OF INVENTION:
FILE OF INVENTION NUMBER: US/10/022,390
CURRENT FILING DATE: 2001-12-17
PRIOR PPLICATION NUMBER: 60/315,382
PRIOR FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 735
SOFTHARE: PSatsEQ for Windows Version 4.0
SEQ ID NO 526
LENGTH: 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Mutant rep protein: rep40 153 398 AGC GCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.9%; Score 72; DB 14; Length 312;
65.0%; Pred. No. 0.003;
iive 3; Mismatches 4; Indels
US-09-953-351-29
US-10-080-376-29
US-10-081-351-29
US-10-097-100-29
US-09-792-631-25
US-09-792-631-25
US-09-792-631-25
US-09-953-351-25
US-09-953-351-25
US-10-080-376-25
US-10-080-376-27
US-10-080-376-27
US-10-080-376-27
US-10-082-671-33
US-10-082-671-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | |:||| | |||||
172 GSAVRVDQKCKSSAQIDPTP 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 65.09
Matches 13; Conservative
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    RESULT 2
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Sequence 523, App
Sequence 523, App
Sequence 523, App
Sequence 29, Appl
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Sequence 524, App
Sequence 524, App
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 525, Appl
Sequence 525, Appl
Sequence 525, Appl
Sequence 525, Appl
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Sequence 525, Appl
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160.719 Million cell updates/sec
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| cgn2_6/ptodata/l/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/l/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/l/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/l/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/l/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/l/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/l/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/l/pubpaa/US08_NEW_PUB.pep:*
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| cgn2_6/ptodata/l/pubpaa/US08_PUBCOMB.pep:*
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| cgn2_6/ptodata/l/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/l/pubpaa/US10A_PUBCOMB.pep:*
| cgn2_6/ptodata/l/pubpaa/US10B_PUBCOMB.pep:*
                                                                                                                                                    May 28, 2004, 12:57:09; Search time 34.75 Seconds
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-022-390-526
US-10-022-249-526
US-10-022-249-524
US-10-022-249-524
US-09-792-630-31
US-10-080-375-31
US-10-080-375-31
US-10-082-671-37
US-10-023-208-31
US-10-023-208-31
US-10-022-249-525
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                                                                                                                                                                                                                                                                                                                                                                                              1151071 seqs, 279249464 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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Sequence 15, Sequence 9,

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Gaps

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Score

Result Š. 1224296911111112

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                 APPLICANT: Drittent, Lila
TILLE OF INVENTION: HIGH THROUGHPUT DIRECTED EVOLUTION BY RATIONAL MUTAGENESIS
FILE REFERENCE: 37851-911
CURRENT APPLICATION NUMBER: US/10/022,249
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/315,382
PRIOR APPLICATION NUMBER: 60/315,382
PRIOR PILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 526
LENGTH: 312
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APPLICANT: Vega, Manuel
APPLICANT: Driteanti, Lila
TITLE OF INVENTION: HIGH THROUGHPUT DIRECTED EVOLUTION BY RATIONAL MUTAGENESIS
FILE REFERENCE: 37851-91
CURRENT APPLICATION NUMBER: US/10/022,249
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 2001-0315,382
PRIOR FILING DATE: 2001-08-27
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APPLICANT: Vega, Manuel
APPLICANT: Drittanti, Lila
APPLICANT: Plaux, Marjorie
TILE REPERENCE: 37851-912
CURRENT APPLICATION NUMBER: US/10/022,390
CURRENT APPLICATION NUMBER: 6071-12-17
PRIOR APPLICATION NUMBER: 607315,382
PRIOR PLING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 524
LENGTH: 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.9%; Score 72; DB 14; Length 397; 65.0%; Pred. No. 0.0039; tive 3; Mismatches 4; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 524, Application US/10022249; Publication No. US20030134351A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 GSAVRVDOKCKSSAOIDPTP 191
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                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 65.Um
Thes 13; Conservative
APPLICANT: Vega, Manuel APPLICANT: Drittanti,
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US-10-022-249-524
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Sequence 31, Application US/09953351
Publication No. US20030036643A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Min
APPLICANT: Liu, Hong-Xiang
APPLICANT: Jiu, Hong-Xiang
CURRENT FILING DATE: 2001-09-14
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Patent No. US20020168640A1

GENERAL INFORMATION:

APPLICANT: Li, Min

APPLICANT: Li, Min

TITLE OF INVENTION:

FILE REPERINCE: A-70295/RFT/RMS/RMK

CURRENT APPLICATION NUMBER: US/09/792,630

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patentin version 3.1

LENGTH: 461
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Pred. No. 0.0046;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                 Length 397;
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                                                                                                                                                                                                                          Score 72; DB 14;
Pred. No. 0.0039;
3; Mismatches 4
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 524
LENGTH: 397
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                                                                                                                                                                                                                                                                                                                                                 172 GSAVRVDQKCKSSAQIDPTP 191
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                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                              Query Match 69.9%;
Best Local Similarity 65.0%;
Matches 13; Conservative
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ilarity 70.0%;
Conservative
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US-09-792-630-31
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Best Local Similarity 70.0°
Matches 14; Conservative
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US-09-953-351-31
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Best Local Similarity
Matches 14; Conserv
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US-09-792-630-31
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APPLICANT: Melander, Christian
APPLICANT: Liu, Hong-Xiang
APPLICANT: Liu, Hong-Xiang
APPLICANT: Liu, Cheng He
TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR THE CONSTRUCTION AND USE OF FUSION L)
FILE REFERENCE: A-70814/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/097, 100
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US/09/953,351
PRIOR APPLICATION NUMBER: US/09/953,351
PRIOR APPLICATION NUMBER: US 60/232,960
PRIOR PILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 461
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APPLICANT: Vega, Manuel
APPLICANT: Drittanti, Lila
APPLICANT: Flaux, Mariorie
TITLE OF INVENTION: MOTANT RECOMBINANT ADENO-ASSOCIATED VIRUSES
FILE REFERENCE: 37851-912
CURRENT APPLICATION NUMBER: US/10/022,390
CURRENT FILING DATE: 2001-12-17
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69.9%; Score 72; DB 14; Length 461;
Best Local Similarity 70.0%; Pred. No. 0.0046;
Matches 14; Conservative 2; Mismatches 4; Indels
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Pred. No. 0.0046;
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US-10-023-208-31
; Sequence 31, Application US/10023208
; Publication No. US20030124537A1
; GENERAL INFORMATION:
; APPLICANT: Li, Min
; APPLICANT: Li, Win
; TITLE OF INTENTION: PROCARYOTIC LIBRARIES AND USES; FILE REFERENCE: A-70174-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/023,208
; CURRENT FILING DATE: 2001-12-17
; PRIOR RIPLICATION NUMBER: US 60/256,163
; PRIOR FILING DATE: 2000-12-14
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PRIOR FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 735
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SOFTWARE: Patentin version 3.1
SEQ ID NO 31
LENGTH: 461
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US-10-023-208-31
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US-10-097-100-31
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Publication No. US20030049647A1
GENERAL INFORMATION:
APPLICANT: DAHTYAT, BASSIL
APPLICANT: DAHTYAT, BASSIL
APPLICANT: LI, MIN
TITLE OF INVENTION: USE OF NUCLEIC ACID LIBRARIES TO CREATE TOXICOLOGICAL
TITLE OF INVENTION: PROFILES
FILE REFERENCE: XEN/001
CURRENT APPLICATION NUMBER: 60/270,781
PRIOR APPLICATION NUMBER: 60/270,781
PRIOR PILLING DATE: 2002-05-17
PRIOR PILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                          Sequence 31, Application US/10080376
Bublication No. US/20020172968A1
GENERAL INFORMATION:
APPLICANT: Li, Min
APPLICANT: Dahiyat, Bassil I.
TITLE OF INVENTION: BIOCHIRS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES
FILE REFERENCE: A-70295-2/FRFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/080,376
CURRENT PILING DATE: 2000-02-19
PRIOR RILING DATE: 2001-02-22
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Pred. No. 0.0046;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 GSAVRVDQKCKGSVCIEPTP 251
                                                           232 GSAVRVDQKCKGSVCIEPTP 251
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                                1 GOAIRIDOKGKGSKQIEPTP 20
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 3.1
LENGTH: 461
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ORGANISM: goose parvovirus
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; ORGANISM: goose parvovirus
US-10-082-671-37
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Matches 14; Conserv
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US-10-082-671-37
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US-10-097-100-31
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US-10-080-376-31
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LENGTH: 461
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APPLICANT: Li, Min

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US-09-792-630-29
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APPLICANT: Vega, Manuel
TITLE OF INTENTION: HIGH THROUGHPUT DIRECTED EVOLUTION BY RATIONAL MUTAGENESIS
FILE REFERENCE: 37851-91
CURRENT APPLICATION NUMBER: US/10/022,249
CURRENT FILING DATE: 2001-12-17
PRIOR FILING DATE: 2001-08-27
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APPLICANT: Vega, Manuel
APPLICANT: Printanti, Lila
APPLICANT: Printanti, Lila
APPLICANT: Printanti, Lila
TITLE OF INVENTION: MISTORIE
FILE REFERENCE: 37851-912
CURRENT APPLICATION NUMBER: US/10/022,390
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/315,382
PRIOR PILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 523
LENGTH: 621
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                                                                                                                             OTHER INFORMATION: Mutant rep protein: rep68 153 398 AGC GCG
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; OTHER INFORMATION: Mutant rep protein: rep78 153 398 AGC GCG US-10-022-390-523
                                                                                                                                                                                          69.9%; Score 72; DB 14; Length 536; 65.0%; Pred. No. 0.0054; Live 3; Mismatches 4; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 525 LENGTH: 536
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SOFTWARE: PartSEQ for Windows Version 4.0
SEQ ID NO 525
LENGTH: 536
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Publication No. US20030134351A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                     ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 65.0
Matches 13; Conservative
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US-10-022-390-523
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publication No. US20030134351A1

Subjection No. US20030134351A1

Subjection No. US20030134351A1

GENERAL INFORMATION:

APPLICANT: Vega, Manuel

APPLICANT: Drittanti, Lila

TITLE OF INVENTION: HIGH THROUGHPUT DIRECTED EVOLUTION BY RATIONAL MUTAGENESIS

FILE REFERENCE: 37851-911

CURRENT APPLICATION NUMBER: US/10/022,249

CURRENT FILING DATE: 2001-12-17

PRIOR FILING DATE: 2001-827

NUMBER OF SEQ ID NOS: 735

SOFTWARE: PASSEG for Windows Version 4.0

SEQ ID NO 523

LENGTH: 621
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Patent No. US20020168640A1
GENERAL INFORMATION:
GENERAL INFORMATION:
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APPLICANT: Li, MI
APPLICANT: Li, MI
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; OTHER INFORMATION: Mutant rep protein: rep78 153 398 AGC GCG
US-10-022-249-523
Score 72; DB 14; Length 621;
Pred. No. 0.0063;
3; Mismatches 4; Indels
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Job time: 34.75 secs
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          Query Match
Best Local Similarity 65.0%;
Matches 13; Conservative
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